Human Sta Human STA Human Sta Human exp Human exp Human exp Human exp Truncated Human STA Antipeori Protein S

Sta STA Sta

Human

exp

Human Human Human Human Human Human Human

Aaw63170
Abu04747
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Adi32352
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Aar41334
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Aaw63168

Perfect score:

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The present sequence is mouse Stat3 protein fragment containing 1-154 amino acids of Stat3 protein. This Stat3 fragment showed very weak binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular
                                                                                                                                                                                                                                                                                                          Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                /note= "Stat3-c-Jun interaction region 1"
                                                                                                                                                                                                                                                                                         Mouse Stat3 protein fragment #1 (1-154 amino acids).
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/note= "N-terminal domain"
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                        ABU04747
ABU04735
                                         ABU04745
ABU04743
ADH57035
                                                                  ADJ32352
ADN04464
AAN84356
AAR41334
ABR04740
AAR72078
AAR72078
AAR72094
                 4AW62995
                                                                                                                                                AAE15172
                                                                                                                                                         AAG78525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 65; Page 66-67; 86pp; English.
                                                                                                                                                                  ABP98871
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                      AAY72840 standard; protein; 154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-AUG-2000; 2000WO-US023822
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Zhang X, Horvath C,
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WO200116605-A2
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AAY72840;
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Aay72840 Mouse Sta
Aar72082 Mouse Sta
Aaw03176 Mouse STA
Aab12377 N-termina
Aae14652 Murine ST
Abul0476 Mouse STA
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Human Pro
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Human PRO
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Mouse Sta
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84 kD ISG
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                                                          5, 2005, 14:55:35 ; Search time 47.8306 Seconds (without alignments) 1245.251 Million cell updates/sec
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                                                                                                             MAQWNQLQQLDTRYLKQLHQ.....AVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                           Description
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Aae22056
Aar82993
Aar82993
Aay03768
Aay03768
Aab19964
Aae15174
Add44738
Add44740
Add44740
Adb64789
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Aar41335 4
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Aae22055
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        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                         2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                           protein search, using sw model
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ABB57164
AAE22054
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AAR82995
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ADD44740
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AAR41335
ABU04741
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AAB12377
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ABU10476
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ABG69497
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ADP54789
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Gapop 10.0 , Gapext 0.5
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    geneseqp1980s:*
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    geneseqp2001s:*
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2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                     Signal transduder and activator of transcription, STAT, 19sf6, Stat3, receptor recognition factor; transcription factor; cellular debilitation; derangement; dysfunction; interferon-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.
                                                                                                                                                                               LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                         9
                                                                                                                                      transformation; These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. Stat protein comprises the N-terminal domain, colled-coil domain, DNA binding domain; linker domain, SH2 domain and transactivation domain
                                                                                                                       1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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                                                                                Length 154;
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                                                                              tch al Similarity 100.0%; Score 800; DB 4; al Similarity 100.0%; Pred. No. 1.1e-77; 154; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                          TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                                                                                                                                                                                                           AAR72082 standard; protein; 770 AA
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93US-00126595.
94US-00212184.
94US-00212185.
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(first entry)
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N-PSDB; AAQ89340.
                                                                                 Query Match
Best Local Similarity
                                                           Sequence 154 AA;
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11-MAR-1994;
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27-SEP-1995
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                                                                                                                                                                                                            1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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                                                                                                       Gaps
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                                               Length 770;
                                100.0%; Score 800; DB 2; Lengin , 100.0%; Pred. No. 9e-77; winmarches 0; Indels
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/label= DNA binding domain
/note= "Claim 3, page 110"
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                                                                                                             Conservative
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                                               Query Match
Best Local Similarity
Matches 154; Conserv
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Sequence 770 AA;
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Disclosure, Fig 1, 42pp; English.
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                                                                                                          Sequence 770 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New crystals of an N-terminal fragment of a signal transducer and activator of transcription that effectively diffracts x-rays, useful for drug screening and development.
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                                                                     1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                            1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                             Gaps
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                              Length 770;
                         Score 800; DB 2; Dengared. No. 9e-77; 0; Indels
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/label= 3(10) helix of alpha helix 2
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                                                                                                                          121 TAAQOGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                  Query Match
100.0%; Score 800; D
Best Local Similarity 100.0%; Pred. No. 9e-
Matches 154; Conservative 0; Mismatches
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99. .119
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/label= Alpha helix 3
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activation of transcription
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                                                                                                                                                                                                                                                    design; murine.
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Signal transducer and activator of transcription; STAT3; drug development; drug discovery; crystal; inflammation; allergy; asthma; leukaemia; anaemia; neutropaenia; thrombocytopaenia; cancer; obesity; viral disease; growth retardation; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater than 5.0 Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal
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RESULT 7
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         signal transducer and activator of transcription (STAT) proteins for the discovery and development of new drug compounds based on the structural compound that binds to the N-terminal domain of a STAT protein.

Identifying a compound that enhances or diminishes the binding of the dimerity of a compound that enhances or diminishes the binding of the site; or identifying a compound that enhances or diminishes the ability of STAT protein dimers to induce the expression of a gene operably under the control of a promoter containing at least two adjacent weak binding sites for STAT protein dimers. The methods are used for identifying new control of a promoter containing at least two adjacent weak binding sites An antagonist of STAT N-terminal dimeric interactions that a promoter of a gene, could be useful situación in the treatment of diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other hand, an agonist of N-terminal dimeric interactions between STAT dimers, can be used as drugs in the treatment of diseases e.g. anaemia, neutropaemia, thrombocytopaemia, cancer, obessity, viral diseases and growth retardation. The present sequence is murine STAT3 protein
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  for detecting compounds that bind to
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/note= "Residues 79, 83, 86, 90 and 94 contribute to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 contribute to
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77. 96
//label= alpha helix 7
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/label= alpha_helix_3
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/label= alpha_helix_1
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 invention relates to methods
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Best Local Similarity 100.
Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse STAT3 protein
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ABU10476
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transducer and activator of transcription (STAT) protein, where the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the N-terminal domain of the STAT protein to a resolution of greater than 5.0 Angstrom. The methods and compositions are useful for the design and screening of drugs that enhance or inhibit STAT-STAT dimer interactions. The present sequence represents the amino acid sequence of mouse STAT3 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New crystal having an N-terminal domain of a STAT protein performing X-ray crystallographic studies, useful for screening drugs that enhance or inhibit STAT-STAT dimer interactions.
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100.0%; Pred. No. 9e-77;
iive 0; Mismatches 0;
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packing of the coiled-coil"
99. .119
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                                                               99. .113
/label= alpha_helix_8
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                                                                                                                                                                                                                                                                                             23-JAN-1998; 98US-00012710.
24-APR-2000; 2000US-00556273.
                                                                                                                                                                                                                                         19-OCT-2001; 2001US-00045792
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Best Local Similarity 100.
Matches 154; Conservative
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DARNELL J E
KURIYAN J.
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                                                                                                                                      US2003003563-A1
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(DARN/)
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                                                         Region
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Sjogren's syndrome, multiple sclerosis, Addison's disease; epilepsy; polymyositis, theumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion; Statbeta.
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ношо варіепв

Location/Qualifiers Misc-difference 713

713. .714 /note= "Encoded by ACA CCA TTC"

WO200220032-A1

14-MAR-2002

10-SEP-2001; 2001WO-US028254

08-SEP-2000; 2000US-0231212P

(UYSF-) UNIV JOHNS HOPKINS.

Dalton W; Jove R, Yu H, Pardoll D,

WPI; 2002-362218/39. N-PSDB; AAD35066.

Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator transcription 3.

Disclosure; Page 87-89; 94pp; English

\$\frac{1}{2}\$\frac

The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing, thypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia in the lower extremities, infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, trauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for an eliotating a syndrom of an autoimmune disease such as systemic lupus erythematosus, multiple sclerosis, insulin dependent diabetes mellitus, syggenen's syndrome, scleroderma, polymyostitis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirthosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitchingo, gluten-sensitive enteropathy, autoimmune butropenia myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, yndurating or treating chesse which includes sarcomas and chesses, rheumatoid attritis, cirthosis, pemphygus vulgaris, autoimmune thyroiditis, idiopathic proliferative and encedence of such active and oncedence of such and stratis, autoimmune thyroiditis, idiopathic proliferative and oncedence of such as sarcomas and consecuted as such and such carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human

Sequence 720 AA;

ö 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL Gaps ö Length 720; 0; Indels DB 5; Score 792; DB 5; Pred. No. 6e-76; 2; Mismatches 99.0%; Matches 152; Conservative Similarity Query Match Local

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TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154 61 121 121 61 셤 Db ሯ

RESULT

ABB57164 standard; protein; 769

ABB57164;

(first entry) 07-MAR-2002 Mouse ischaemic condition related protein sequence SEQ ID NO:398.

Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease.

Mus musculus.

WO200188188-A2

22-NOV-2001

18-MAY-2001; 2001WO-JP004192.

18-MAY-2000; 2000JP-00145977.

(UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON

Ishii Y; Takahashi Y, Nagata T, Asai S, Ishikawa K,

WPI; 2002-034733/04.

N-PSDB; ABI99454

Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes.

Claim 2; Page 1084-1087; 2690pp; English.

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapbutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention

Sequence 769 AA;

Gaps . 0 Length 769; 0; Indels 99.0%; Score 792; DB 5; 98.7%; Pred. No. 6.5e-76; ive 2; Mismatches 0; Conservative Query Match Best Local Similarity Matches 152;

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9 1 MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 1 MAQWNOLOOLDTRYLKOLHOLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL

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LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120

neutropenia, myasthenia gravis,

idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human Stat3

Sequence 769 AA;

protein

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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stati). Modulating angiogenesis is useful for treating or preventing thypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, coronary atherosclerosis, myocardial infarction, inflammation, corolusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy control as symptom of an autoimmune disease such as systemic lupus exprementosus, multiple sclerosis, insulin dependent diabetes mellitus, cyprentis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
                                                                                                                                                                                                                                                                                                                                                                                                       immune response; Stat3; coronary atherosclerosis; vaccular occlusion; hypoxia; stroke; anglogenesis; myocardial infarction; hypoplycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilopsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.
                                                                                                                                                                                                                                                                                                                                                                                   Human; signal transducer and activator of transcription 3; ischaemia
                                                                    154
                                                                                      121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dalton W;
                                                                                                                                                                                                                AAE22054 standard; protein; 769 AA
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                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                              Human Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-362218/39.
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                                                                             LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA
                                                             1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                               Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; anapisgenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; sjogren's syndrome; multiple sclerosis; Addison's disease; spilepsy; polymyositis; theumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; discease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.
                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a
 Length 769;
                                Indels
 Score 792; DB 5; L
Pred. No. 6.5e-76;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                        Human protein related to angiogenesis regulation.
                                                                                                                                                                                      TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                          TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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Query Match
Best Local Similarity 98.7%;
Matches 152; Conservative
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                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                 RESULT 10
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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transfucer and activator of transcription 3 (Stata). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, tissue ischaemia or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, introgen necroasis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus crythematosus, multiple solerosis, insulin dependent diabetes mellitus, signate onnective tissue disease, primary bilary cirrhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thromborycopenia purpura, Grave's disease, coodpestures and carearist disease. The method is useful in preventing or treating carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, chronic leukaemia, ilposarcoma, disease, method is see which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, thromborycomena, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human cry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
compound that modulates the activity of a signal transducer and activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; acute phase response factor; transcription factor; interleukin-6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 792; DB 5; Length 76
Pred. No. 6.5e-76;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse liver acute phase response factor.
                                                               Disclosure; Page 83-85; 94pp; English
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; acute phase response factor; transcription factor; interleukin-6;
                                                                                                                                                             New acute phase response factor - for developing inhibitory agents for treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
                                                                                                                                                                                                                                                   The sequence represents a mouse acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (I 6). The protein is encoded by a CDNA, isolated from a mouse liver CDNA library using a polymerase chain reaction product (amplified using primers derived from an IL-6-treated mouse liver peptide) as a probe. APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or ribozymes, may be used to treat diseases induced by IL-6, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                        inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   signal transmission; placenta; antibody; antisense; ribozyme; antinflammatory; antitumor; hypotensive; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human placenta acute phase response factor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 792; DB 2;
Pred. No. 6.5e-76;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                              94JP-00065825
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Best Local Similarity 98.7%;
Matches 152; Conservative
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                                                                                      Akira S, Kishimoto T;
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                                                        (KISH/) KISHIMOTO T.
                                                                                                                 WPI; 1995-346089/45
                                                                                                                                                                                                                                                                                                                                                                           hypertension, etc
                                                                                                                                 N-PSDB; AAT05619
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 770 AA;
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                              04-APR-1994;
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29-MAR-1995;
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Length 770; Indels 9 9

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The present sequence represents a predominant allelic variant of human Signal Transducer and Activator of Transcription 3 (STAT3) protein, an intracellular transcription factor which mediates IL-6 signals. The encoding sequence differs from the original published human STAT3 gene sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3 bNA molecule can be used for the recombinant expression of the variant. STAT3 protein is useful as a medicament or pharmaceutical composition for treatment of autoimmune or inflammatory diseases
                                                                                                                                                                                                                                                                                                                                   LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                                                  LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                    1 MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human signal transducer and activator of transcription STAT-3.
                                                                                                                                                                                               Score 792; DB 2; L
Pred. No. 6.5e-76;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                       121 TAAOOGGOANHPTAAVVTEKOOMLEOHLODVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB19964 standard; protein; 770
                                                                                                                                                                                                 99.0%;
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                                                                                                                                                                                                 Query Match
Best Local Similarity 98.7
Matches 152; Conservative
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                                                                                                                                                                 Sequence 770 AA;
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                                                                                                                                                          The sequence corresponds to a human acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (IL-6). The protein is expressed from a human placenta cDNA, isolated using an IL-6-treated mouse liver cDNA probe. APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or ribozymes, may be used to treat diseases induced by IL-6, e.g. inflammatory disease, leukemia, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New acute phase response factor - for developing inhibitory agents for treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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Pred. No. 6.5e-76;
2; Mismatches 0
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                                                                                                                             Claim 3; Page 9-12; 31pp; English
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                                                                                                                                                                                                                                                                                                                            99.0%;
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Matches 152; Conservative
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            1995-346089/45
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STAT-3; signal transducer and activator of transcription 3; human;
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                                                                                                                                                                                                                                                              "C-terminal tail segment"
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N-PSDB; AAA89229.
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New human Signal Transducer and Activator of Transcription 3 (STAT3) allelic variant useful for treatment of autoimmune and inflammatory

Claim 2; Page 9-13; 32pp; English

disease

Homo

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transcription 3 (STAT-3). The invention provides a crystal of a core portion of a STAT protein in dimer form with an 18-mer duplex DNA (see AAA89233) that contains a binding site for the STAT dimer. The core portion comprises a colled-coil domain comprising 4 long helices, a DNA binding domain which contains an immunoglobulin-like fold, a C-terminal crystal is of sufficient quality to perform X-ray crystallography studies. Methods of preparing the crystals are included in the invention. Knowledge of the STAT protein's 3-dimensional structure will aid in structure-based drug design. The crystal can be used in drug screening assays to identify agonist and antagonist compounds. Antagonists can be used to treat inflammation, allergy, asthma and leukaemia, and agonists core treat anaemia, neutropenia, thrombocytopenia, cancer, obesity, viral diseases, growth retardation, and other conditions characterized by insufficient STAT activity
                                                                                                                                              present sequence is that of human signal transducer and activator of
Novel crystal useful in drug screening assays, comprises portion of signal transducer, activator of transcription and duplex DNA.
                                                                                       Disclosure; Col 67-71; 206pp; English
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Sequence 770 AA;

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LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                             MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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                                      0; Gaps
Query Match 99.0%; Score 792; DB 4; Length 770; Best Local Similarity 98.7%; Pred. No. 6.5e-76; Matches 152; Conservative 2; Mismatches 0; Indels
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ABG69497 standard; protein; 770 AA (first entry) Human bait protein STAT3. 21-OCT-2002 Homo sapiens ABG69497; RESULT 15 ABG69497

Human, yeast two-hybrid assay, adipocyte, bait protein; NIDDM, non-insulin diabetes mellitus, obesity, selected interacting domain, SID, protein-protein interaction map; PIM, anorectic, metabolic disorder.

WO200253726-A2.

11-JUL-2002.

28-DEC-2001; 2001WO-EP015423

02-JAN-2001; 2001US-0259377P

(HYBR-) HYBRIGENICS. (CNRS) CENT NAT RECH SCI

Jockers R; Legrain P; Marullo S,

WPI; 2002-583612/62 N-PSDB; ABS51033

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The invention relates to a complex of protein interactions

(forming a protein-protein interaction map, PIM) in adipocyte cells as

defined in the specification, or polynucleotides in adipocyte sencoding

Co the polypeptides. Also included are a recombinant cell expressing the

interacting polypeptides and a method of selecting a modulating compound

in adipocyte cells, by cultivating a recombinant host cell on a selective

compound in the toward for the recombinant host cell on a selective

compound with two vectors, where the first vector comprises a

compound with two vectors, where the first vector comprises a

compound the second vector comprising a polynucleotide encoding a second

hybrid polypeptide and an activating domain that activates the toxic

creporter gene, when the first hybrid polypeptides interact and

crecombinant host cell (i.e. using the yeast two-hybrid system). The

crecombinant host cell (i.e. using the yeast two-hybrid system). The

complexes are useful for identifying compounds that modulate the protein-

crecombinant host cell (i.e. using the yeast two-hybrid system). The

complexes are useful for identifying compounds that modulate the protein-

crecombinant host cell (i.e. using the yeast two-hybrid system). The

compound isolated by the method is useful for treating and preventing

compound isolated by the method is useful for treating and preventing

cobesity or metabolic diseases. The interactions between the proteins of

the complex sequence represents a member of the protein complex of the

compound, used as the bait protein in the yeast two-hybrid assay
Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders.
                                                                                                                            Claim 1; Page 54; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 770 AA;
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invention.

ö 0; Gaps Length 770, 0; Indels Score 792; DB 5; Pred. No. 6.5e-76; 2; Mismatches 0. 99.0%; Query Match Best Local Similarity 98.7³ Matches 152, Conservative

1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL

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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120 1 MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60 g ઠે 셤

TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154 121 ò 셤

121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154

completed: May 5, 2005, 15:01:09 Job time : 50.8306 secs Search

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-369-796-12

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US-08-856-652-12

US-08-956-869-12

US-09-36-8912

US-09-364-970-3

US-09-364-970-3

US-09-364-970-3

US-09-366-273-8

US-09-556-273-8

US-08-956-653A-12

US-08-956-273-8

US-08-972-800A-6

US-09-972-800A-6

US-09-972-800A-6

US-09-972-800A-14

US-08-117-087-2

US-09-972-800A-14

US-08-111-087-2

US-09-972-800A-14

US-08-972-800A-14

US-08-973-800A-14

US-08-973-800A-14
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12 3 US-08-956-652-6 Sequence 6, Appli	ALIGNMENTS	USE 18 APPLICATION US/09387418A Gequence 8, Application US/09387418A APPLICANT: Marseszczynska, Melissa H APPLICANT: 159 CURRENT APPLICATION NUMBER: US/09/387,418A CURRENT APPLICATION NUMBER: 1999-08-31 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 GRQANISM: Mus musculus ORGANISM: Mus musculus OGRGANISM: Mus musculus	100.0%; Score 800; DB 3; Length 154; ty 100.0%; Pred. No. 7.3e-79; Indels 0; Gaps 0;	MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60 	LGEIDOQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKBMEIARIVARCIMEESRLLQTAA 120 	TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154 	SULT 2 -08-369-796-12 Sequence 12, Application US/08369796 Parent No. 5716622 GENERAL INFORMATION: APPLICANT: James E. Darnell, Jr.
24444444444444444444444444444444444444		Application US/0 391572 391572 391572 Zhang, Xiaokui Wrzeszczynska, Horvath, Curt M Darnell Jr., Ja VENTION: METHOD VENTION: METHOD VENTION: 107ERA NCE: 600-1-253 LICATION NUMBER: LIGATION NUMB	ilarity Conservat	aqwnqlqqldtr aqwnqlqqldtr	GEIDQQYSRFLQ GEIDQQYSRFLQ	aaqqgganhpt aaqqgganhpt	2 Application 16622 RMATION: James E. D
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APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Zilong Wen
APPLICANT: Zhong Zilong Wen
APPLICANT: Zhong Zhong
TITLE OF INVENTION: TRANSDUCER AND ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS

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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Weng Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
FILING DATE: 11-MAR-1994
PatentIn Release #1.0, Version #1.25
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06-MAY-1997
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SYSTEM: PC-DOS/MS-DOS
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Matches 154; Conservative
                           CURRENT APPLICATION DATA
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Jersey
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  SOFTWARE:
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Patent No. 588328
GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Zhong Zhong
APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 800; DB 1; Length 770; 100.0%; Pred. No. 5.9e-78; tive 0; Mismatches 0; Indels
                                                                                                                                                                                  COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
ATTONEX/AGENT INFORMATION:
NAWE: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION 1NFORMATION:
TELEPOMMUNICATION 1NFORMATION:
TELEPOMMUNICATION 1NFORMATION:
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TELEPOMMUNICATION 1NFORMATION:
TELEPOMMUNICATION 1000
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COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"TWOTTER: IBM PC COMpatible
"TWOTTER: FORM: PC-DOS/MS-DOS
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CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-369-796-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
                                                                                           CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
  NUMBER OF SEQUENCES:
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TELEX: 13
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            us-08-956-652-12
; Sequence 12, Application US/08956652
; Patent No. 6013475
; GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Harber
GITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 800; DB 2; Length 770; 100.0%; Pred. No. 5.9e-78; tive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
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                                                                                                                                                                                                                                                                  NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                  PRICE AND DATE:

APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SER-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
APPLICATION NUMBER: US 0'
FILING DATE: 23-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 154; Conservative
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; MOLECULE TYPE: protein
US-08-820-754-12
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 800; DB 3; Length 770; 100.0%; Pred. No. 5.9e-78;
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                                                       APPLICATION NUMBER: US US/112,185
FILING DATE: 11-WAR.1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR.1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR.1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 19-WAR.1993
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESQ., David A.
REGISTRATION NUMBER: 26,742
FELEFRAX: 201 343-1684
TELEFRAX: 201 343-1684
TELEFRAX: 201 343-1684
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 770 amino acids
amino acid
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Best Local Similarity 100.0
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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26,742
ep. 600-1-194
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  APPLICATION NUMBER: US/09/012,710
               FILING DATE:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKEY NUMBER: 600-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-343-1684
TELERA: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids

LENGTH: 770 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAQWNQLQQLDTRYLKQLHQLYSDTFPWELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps.
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Patent No. 6087478
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
APPLICANT: Moarefi, Ismail
APPLICANT: Moarefi, Ismail
APPLICANT: Moarefi, Ismail
APPLICANT: Kuriyan, John
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                                                             APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR-1992
RIGH APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
RIGH APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...uksSE: ...uksSS:
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
APPLICATION NUMBER: US/08/956,869
                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/212,185
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 133521
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7770 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-956-869-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                          61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPWEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                     1 MAÇWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
                                                                                                                                                1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
Query Match 100.0%; Score 800; DB 3; Length 770; Best Local Similarity 100.0%; Pred. No. 5.9e-78; Matches 154; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Xian-Yuan
APPLICANT: Abong, Zhong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/948,547

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/212,185

FILING DATE: 11-MAR-1994

APPLICATION NUMBER: US 07/980,498
                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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COUNTRY: USA
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                                                                                                                                                                                                                          -09-364-970-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
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APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REPERBRÜCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE PATENTIAL OF THE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMULCATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFRAX: 201 343-1684
                              FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
US 07/854,296
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Patent No. 6235873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 770 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: mino acid
TYPE: protein
US-08-948-547-12
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Best Local Similarity 100.
Matches 154; Conservative
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Best Local Similarity 100.
Matches 154; Conservative
   APPLICATION NUMBER:
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ORGANISM: Mus musculus
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-282
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT AILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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APPLICANT: Vinkemeler, Uwe
APPLICANT: Moarefi, Ismail
APPLICANT: Moarefi, Ismail
APPLICANT: Darnell, Jr., James E.
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
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100.0%; Score 800; DB 3;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0;
121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                               121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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APPLICATION NUMBER: US/09/556,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1 0
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APPLICATION NUMBER: 09/012,710
FILING DATE:
                                                                                                                                                                                     Sequence 5, Application US/09364970
Patent No. 6235873
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; Sequence 8, Application US/09556273
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CRGANISM: Mus musculus
US-09-364-970-5
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CLASSIFICATION:
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APPLICATION NUMBER:
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APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Fu, Xian-Yuan
APPLICANT: Talong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Harber
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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SOFTWARE: PARCHETIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,653A
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 800; DB 3;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0;
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
RPLICATION WUMBER: US 07/980,498
FILING DATE: 13-NOV-1992
PRIOR APPLICATION DATA:
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
                     NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/0895653A
Patent No. 6338949
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                  TELEX: 133521
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
ATTORNEY/AGENT INFORMATION NAME: Jackson Esq., Davi
                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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I. No. 5.9e-78;
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APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Pu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
PAPLICATION NUMBR: US/08/212,185
FILING DATE: 11-MAR.-1994
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100.0%; Score 800;
Best Local Similarity 100.0%; Pred. No. 5
Matches 154; Conservative 0; Mismatche
                  FILING DATE: 19-MAR-1993
RRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/126,588
FILING DATE: 24-SEP-1993
ATORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26/742
REFERENCE/DOCKET NUMBER: 600-1-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 343-1684
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION NUMBER: US 07/854,296
APPLICATION NUMBER: US 07/854,296
MBER: WO US93/02569
19-MAR-1993
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...ES
...DRESS:
...LKET: Klauber & Jackson
...KEET: 411 Hackensack Avenue
CTTY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 0760'
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08212185
Patent No. 660542
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             : 770 amino acids
amino acid
                                                                                                                                                                                                                                                                                               TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-956-653A-12
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, MOLECULE TYPE: protein US-08-416-5818-1
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PCT-US95-17025-12
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APPLICANT: Jilong Wen
APPLICANT: Cutr M. Horvath
APPLICANT: Cutr M. Horvath
APPLICANT: Cutr M. Horvath
APPLICANT: Chong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STREET: 411 Hackensack
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 · LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 800; DB 4;
Pred. No. 5.9e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELECHONE: 201 487-5900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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28-DEC-1995
V:
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APPLICANT: James E. Darnell, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                TELEX: 133521
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 154; Conservative
                                                                                                                                                                                                                                                 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-212-185-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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Best Local Similarity
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TELEGRANG TO COCKET NUMBER 6 60-1-116
TELEGRANG 210 487-5500
TELEGRANG 210 497-5500
TELEGRA
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Query Match
Best Local Similarity 98.7%; Pred. No. 4.3e-77;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAQWNQLQQLDTRYLEQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60

Qy 61 LGELDQQYSRFLQESVVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120

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Search completed: May 5, 2005, 14:58:51 Job time: 26.1906 secs

121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154

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5, 2005, 14:59:00 ; Search time 64.8612 Seconds (without alignments) 792.064 Million cell updates/sec
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1 MAQWNQLQQLDTRYLKQLHQ.....AVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*

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12: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*

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16: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
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(cgn2_6/ptodata/2/pubgaa/0310860_NBW_PUB.ppp:

(cgn2_6/ptodata/2/pubgaa/0310860_NBW_PUB.ppp:
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1428581 seqs, 333598853 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%,
Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                              US-10-090-185-8
                                                                                                                                                                                               May
                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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                                                                                                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 8, Appli	Sequence 12, Appl	Sequence 8, Appli	Sequence 12, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 56, Appl	Sequence 2, Appli	329		Sequence 780, App	Sequence 780, App	
	ΩI	US-10-090-185-8	US-09-876-773-12	US-10-045-792-8	US-10-639-617-12	US-10-380-020-4	US-10-380-020-2	US-10-380-020-5	US-10-038-010-56	US-10-117-087-2	US-10-116-275-329	US-10-116-275-349	US-09-925-302-780	US-09-925-302-780	
	DB	13	11	14	17	15	15	15	14	14	15	15		10	
	Query Match Length DB ID	154	770	770	770	720	769	769	770	770	770	770	793	793	
*	Query Match	100.0	100.0	100.0	100.0	99.0	0.66	0.66	99.0	0.66	0.66	0.66	0.66	0.66	
	Score	800	800	800	800	792	792	792	792	792	792	792	792	792	
	Result No.		7	m	4	2	9	7	80	σ	10	11	12	13	

7,6,7	Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 4, Appli	1, 44, 352	823, 19, 7 4, Ap	ξ. γ.	Sequence 8, Appli Sequence 7, Appli	J 00 4.	10, 10, A, A	Sequence 437, App Sequence 439, App Sequence 70, Appl	38,	
10-090-185 09-876-773 10-245-120	17 US-10-639-617-6 17 US-10-936-390-5 9 US-09-833-205-2 11 US-09-876-773-4	US-10-245-120 US-10-308-279 US-10-755-889	US-10 US-10 US-10	9 US-09-925-297-550 9 US-09-833-205-4 9 US-09-833-205-6	US-09-876-773-8 US-10-045-792-7	US-10-205 US-10-639 US-10-245	US-09-876-773-1 US-10-639-617-1 US-10-045-792-9	14 US-10-177-293-437 14 US-10-177-293-439 16 US-10-755-889-70	16 US-10-755-889-362 14 US-10-205-823-389 11 US-09-876-773-2	
154 712 712	712	750 750 750	750 750 750	786 749 749	749	749 749 131	748 748 749	423 748 748	748 532 851	851 851
2.7.4 47.5 2.7.5	7 4 4 4 4 4 4 7	. 4 4 4 	47.5 47.5 47.5	47.5	47.2	47.2 47.2 45.0	41.8 41.8 41.8	41.7 41.7 41.7	41.7 30.9 30.9	30.9
380	3800	380	380 380 380	380 378 378	378	378 378 360	334.5 334.5 334.5	333.5 333.5 333.5	333.5 247.5 247.5	247.5 247.5
11 11 10 10 10	, 86 C 1 C	22 23 23 23 23	24 25 26	27 28 29	330	33 34 34	35 37 37	338 40 8	41 42 43	44

ALIGNMENTS

RESULT 1 US-10-090-185-8 Sequence 8, A Sequence 8, A Publication N GENERAL INFORM APPLICANT: APPLIC	SULT 1 10-090-185-8 Sequence 8, Application US/10090185 Sequence 8, Application US/10090185 Sequence 8, Application US/200197647A1 GENERAL INFORMATION: APPLICANT: Zhang, Xiaokui APPLICANT: Are zeazczynska, Melissa H APPLICANT: Mrzeazczynska, Melissa H APPLICANT: Mrzeazczynska, Melissa H APPLICANT: Darnell Jr., James E TITLE OF INVENTION: INTERACTIONS TITLE OF INVENTION: INTERACTIONS FILE REFERENCE: 600-1.253 CURRENT APPLICATION NUMBER: US/10/090,185 CURRENT APPLICATION NUMBER: 09/387,418 PRIOR FILING DATE: 1999-08-31 SOUTWARE: Patentin Ver. 2.0 SEQ ID NO 8 LENGTH: 154 TYPE: PRT TYPE: PRT ORGANISM: Mus musculus ORGANISM: Mus musculus
Query Match	Query Match
Best Local	Best Local Similarity 100.0%; Pred. No. 4.7e-77;
Matches 15	Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
çy	1 MAGMNOLOQLDTRYLKOLHOLYSDTFPMELRQFLAPWIESODWAYAASKESHATLVFHNL 60
Dp	
Qy	61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
Dp	

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121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                     121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAOWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
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0
                                                                                                                                                                                                                                         Wen, Zilong
Zhong Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 800; DB 11; Length 770; 100.0%; Pred. No. 3.7e-76; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/212,185

RILING DATE: 11-WAR-1994

APPLICATION NUMBER: US 07/980,498

FILING DATE: 23-NOV-1992

APPLICATION NUMBER: US 07/854,296

FILING DATE: 19-WAR-1992

APPLICATION NUMBER: US 08/126,588

FILING DATE: 19-WAR-1993

APPLICATION NUMBER: US 08/126,588

FILING DATE: 19-WAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:
                     TAAQOGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12
                                                                                                     RESUL: 4

US-09-876-773-12

Sequence 12, Application US/09876773

Publication No. US20040058318A1

GENERAL INFORMATION:

APPLICANT: Darnell Jr., James E.

Schindler, Christian W.
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 411 Hackensack Avenue CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 154; Conservative
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Best Local Similarity
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                                                                        Moarefi, Ismail
Darnell, Jr., James E.
Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 800; DB 14; Length 770; Best Local Similarity 100.0%; Pred. No. 3.7e-76; Matches 154; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/012,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLGGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: <Unknown>
ATTORREY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
US-10-045-792-8; Sequence 8, Application US/10045792; Publication No. US20030003563A1; GENERAL INFORMATION: APPLICANT: Vinkemeier, Uwe
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TELEFAX: 201-343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                   CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 133521
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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APPLICANT: Yu, Hua
APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REPERENCE: 10073-009-999
CURRENT APPLICATION NUMBER: 06/231,212
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 720
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Pred. No. 2.4e-75;
2; Mismatches 0; Indels
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Pred. No. 2.7e-75;
2; Mismatches 0;
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                                          Sequence 4, Application US/10380020 Publication No. US20040052762A1 GENERAL INFORMATION:
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Best Local Similarity 98.7%;
Matches 152; Conservative
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Best Local Similarity 98.7%;
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
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TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEI.
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDLUM TYPE: Floppy disk

CONFUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 12-Aug-2003

CLASSIFICATION NUMBER: US/10/639,617

FILING DATE: 11-Aug-2003

CLASSIFICATION NUMBER: US/08/212,185

FILING DATE: 11-Aug-1994

APPLICATION NUMBER: US 07/980,498

FILING DATE: 19-MAR-1992

APPLICATION NUMBER: US 07/854,296

FILING DATE: 19-MAR-1993

APPLICATION NUMBER: WO US93/02569

FILING DATE: 19-MAR-1993

APPLICATION NUMBER: US 08/126,588

FILING DATE: 19-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: JACKSON ENG. DAVIG A.

REFERENCE/DOCKET NUMBER: 600-1-073 CIP

TELECOMMUNICATION:

APPLICATION INFORMATION:

APPLICATION INFORMATION:
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100.0%; Pred. No. 3.7e-76;
ive 0; Mismatches 0;
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                        STREET: 411 Hackensack Avenue
            Sequence 12, Application US/10639617
Publication No. US20050079543A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E. Schindler, Christian W. Fu, Xian-Yuan
                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
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                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                              CITY: Hackensack
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Best Local Similarity 100.
Matches 154; Conservative
US-10-639-617-12
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APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Datcow, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REPRENCE: 10873-009-999
CURRENT APPLICATION NUMBER: 108/10/380,020
CURRENT FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR PLILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 769 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120 1 MAQWNQLQQLDTRYLEQLHQLYSDSFFWELRQFLAPWIESQDWAYAASKESHATLVFHNL 60 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL Gaps ö Length 769; 0; Indels ò

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Query Match
Best Local Similarity 98.74
Matches 152; Conservative
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US-10-117-087-2
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APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Daton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REPERENCE: 10813-009-999
CURRENT APPLICATION NUMBER: 60/231,212
PRIOR FILING DATE: 2003-099
PRIOR FILING DATE: 2003-09-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEJARIVARCLWEBSRLLQTAA 120
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| Publication No. US20030040089A1
| GENERAL INFORMATION:
| APPLICANT: HYBRIGBURCS
| APPLICANT: Pierre, Legrain
| TILLE OF INVENTION: Protein-protein interactions in adipocyte cells
| FILE REFERENCE: B4767A
| CURRENT FILING DATE: 2002-07-23
| PRIOR PILING DATE: 2002-07-23
| PRIOR FILING DATE: 2001-01-02
| NUMBER OF SEQ ID NOS: 67
| SOFTWARE: Patentin version 3.1
| SEQ ID NOS: 67
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Pred. No. 2.7e-75;
2; Mismatches 0;
                                                                              121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                                                                                                        Sequence 5, Application US/10380020
Publication No. US20040052762A1
GENERAL INFORMATION:
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Matches 152; Conservative
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ORGANISM: Homo Sapiens
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LENGTH: 769
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APPLICANT: Byrne, Daragh
APPLICANT: Lambkin, Imedia
APPLICANT: Lambkin, Imedia
APPLICANT: Higgins, Insel
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn version 3.1
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Score 792; DB 14; Length 770;
Pred. No. 2.7e-75;
2; Mismatches 0; Indels (
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APPLICANT: DELLA PIETRA, Linda
TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
FILE REPERENCE: SERLUPI-2
CURRENT APPLICATION NUMBER: US/10/117,087
CURRENT FILING DATE: 2002-04-08
FRIOR APPLICATION NUMBER: US/09/526,542
FRIOR APPLICATION NUMBER: US/09/526,542
NUMBER OF SEQ ID NOS: 19
SOPTWARE: Patentin Version 3.0
SEQ ID NO 2
LENGTH: 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 792; DB 14;
Pred. No. 2.7e-75;
2; Mismatches 0;
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Publication No. US20030166854A1
GENERAL INFORMATION:
         99.0%;
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Best Local Similarity 98.7%;
Matches 152; Conservative
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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Sequence 780, Application US/09925302

Sequence 780, Application US/09925302

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

TILE REFERENCE: PA.04

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

SOFFWARE: PATENTIN VENER: 60/124,270

SOFFWARE: PATENTIN VENER: 2007-03-03-12
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99.0%; Score 792; DB 9; L
Best Local Similarity 98.7%; Pred. No. 2.8e-75;
Matches 152; Conservative 2; Mismatches 0;
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/USO0/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 780
LENGTH: 793
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; Sequence 11, Application US/10090185
; Publication No. US20020197647A1
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Best Local Similarity 98.7%;
Matches 152; Conservative
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US-09-925-302-780
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US-09-925-302-780
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LENGTH: 793
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APPLICANT: O'Mahony, Daniel J.
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Higgins, Liea
APPLICANT: Momeorial Rargeting Peyer's Patches and Mchods and TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors FILE REFERENCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn version 3.1
SEQ ID NO 349
LENGTH: 770
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99.0%; Score 792; DB 15; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.7e-75;
Matches 152; Conservative 2; Mismatches 0; Indels
                                                                                                                                                     Length 770;
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Patent No. US20020044941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
                                                                                                                                                                                                  Indels
                                                                                                                                              Query Match 99.0%; Score 792; DB 15; Best Local Similarity 98.7%; Pred. No. 2.7e-75; Matches 152; Conservative 2; Mismatches 0;
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-09-925-302-780
                                                 ; TYPE: PRT
; ORGANISM: Rat
US-10-116-275-329
    SEQ ID NO 329
LENGTH: 770
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61 LSQLDDQYSRFSLENNFLLQHNIRKSKRNLQDNFQEDPIQMSMIIYSCLKEERKILENAQ 120
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                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
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                                 FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
APPLICATION NUMBER: WO US93/02569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-876-773-6
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te : 65.8612 secs
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TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 712 amino acids
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Job time :
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                                                                                         APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James B
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 2002-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Indels
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; Pred. No. 2.5e-32;
42; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | : : : | : : |: : | : : | : : | | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : : | : : | : : | : : : | : : : | : : : | : : | : : : | : : | : : : | : : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
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FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
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Publication No. US2004058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian Yuan
Wen, Zilong
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ADDRESSEE: Klauber & Jackson
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                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VEY. 2.0
SEQ ID NO 11
LENGTH: 154
                                                           Wrzeszczynska, Melissa H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.58;
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COMPUTER READABLE FORM:
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Best Local Similarity 44.8*
Matches 69; Conservative
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STATE: New Jersey
                          Zhang, Xiaokui
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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1;

Gaps 2;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

5, 2005, 14:55:35 ; Search time 11.2329 Seconds (without alignments) 1319.101 Million cell updates/sec May Run on:

US-10-090-185-8 800 1 MAQWNQLQQLDTRYLKQLHQ......AVVTEKQQMLEQHLQDVRKR 154 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		•			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID.	Description
-	792	0.66	770	٦,	A54444	DNA-binding protei
7	792	o O	770	7	ഥ	
٣	380		739	7	A46159	interferon-depende
4	334.5	41.8	748	7	A56047	gamma-interferon a
S	247.5	。	851	~	A46160	interferon alpha-i
9	188		786	7	149274	
7	187	23.4	794	7	G02317	
œ	186	23.2	793	~	S54772	mammary gland fact
6	147.5	18.4	794	7	855527	01
10	96	12.2	331	~	AI0354	Ω
11	97	12.1	837	7	157557	
12	91.5	11.4	848		A54740	interleukin-4-indu
13	88	11.0	1355		T22552	hypothetical prote
14	82.5	10.3	371	•	T40287	cal
15	82.5	10.3	373	•	F71884	probable lipopolys
16	82	10.2	498		C69587	L-arabinose isomer
17	82	10.2	620	7	S56790	probable membrane
18	82	10.2	764		C83513	hypothetical prote
19	81.5	10.2	276		H81707	inclusion membrane
20	81	10.1	2954		T14156	ro.
21	80.5	10.1	1110		A43253	Large tra-1 protei
22	80	10.0	508		KRSHL2	keratin type II, m
23	79.5	9.9	392		T19867	 hypothetical prote
24	79.5	9.9	444		E90192	н
25	79.5	9.6	613		S48557	hypothetical prote
26	79.5	9.9	638	7	153169	cytokeratin 2 - hu
27	79.5	9.9	4957		T03455	ı
28	79.5	9.6	5262		345	
59	79	9.6	4540	~	T30838	 cytoplasmic dynein

MG328 homolog P01_	nuclear mitotic ap	ninein - mouse	hypothetical prote	keratin, 65K type	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	probable transcrip	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	probable alpha-act	probable alpha-act
S73693	A42184	T30171	F71956	A29666	T00345	T30637	AB2247	T20241	T37604	A72108	B86514	C83192	T34180	T13414	T13413
7	N	~	~	~	~	~	~	7	N	~	~	~	N	~	7
1033	2101	2168	409	629	1462	2133	191	2160	625	390	390	442	812	895	924
9.	9.8	9.8	9.6	9. 8	9. 8.	9.7	9.6	9.6	9.6	9.5	9.5	9.5	9.5	9.4	4.
78.5	78.5	78.5	78	78	78	77.5	77	77	76.5	16	92	16	92	75.5	75.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 A54444 DNA-binding protein APRF - human
	lomo sapiens (
	C.ACCESBION: A34444 C.Akira, S., Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sudr Call 77 63-71 1994
	A; Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tra- A; Reference number: A54444; MUID:94208062; PMID:7512451
	A;Accession: A54444 A;Status: preliminary; translated from GB/EMBL/DDBJ
	A;Molecule type: mRNA A;Mesidues: 1-770 c.RES. A;Trose_reference: IMIPEOT.p40763: GR:129277: NID:c475788: PID:c475789
	C;Superfamily: human signal transducer and transcription activator STAT5A C;Keywords: DNA binding; transcription factor
	Query Match 99.0%; Score 792; DB 2; Length 770; Best Local Similarity 98.7%; Pred. No. 1.1e-61; Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
	OY 1 MAQMNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
	Db 1 MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
	Qy 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
	Db 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
	Qy 121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
	Db 121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
_	RESULT 2 149508
	ISGP3 p91-related transcription factor - mouse C.Species: Mus musculus (house mouse) C.Dato. 02-11-1-1064 #semmence revision 02-11-1-1994 #fext change 08-11-1-2004
	C; Accession: 149508; 149009 R; Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sud
	Cell 77, 63-71, 1994
	A;Status: preliminary; translated from GB/EMBL/DDBJ
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Conservative
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Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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A;Residues: 1-851 <YAN>
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       C; Accession: A56047
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A,Residues: 1-770 <RES>
A,Cross-references: UNTROOT:P42227; GB:L29278; NID:g476715; PIDN:AAA37254.1; PID:g476716
A,Cross-references: UNTROOT:P42227; GB:L29278; NID:g476715; PIDN:AAA37254.1; PID:g476716
B,Raz, R.; Dubrin, J.E.; Levy, D.B.
J. Biol. Chem. 269, 24391-24395, 1994
A,Title: Acute phase response factor and additional members of the interferon-stimulated A,Reference number: 149009; MUID:95014185; PMID:7523373
A,Reference number: preliminary; translated from GB/EMBL/DDBJ
A,Rolecule type: mRNA
A,Residues: 1-393, M', 395-700, 702-770 <RE2>
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C;Species: Homo sapiens (man)
C;Date: 21.569-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 21.569-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R;Schindler, C.; Fu, X.Y.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa A;Reference number: A46159, MUID:92366557; PMID:1502203
A;Accession: A46159
A;Accessio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEXPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAQWINGLOOLDTRYLKOLHOLYSDTFPMELROFLAPWIESQDWAYAASKESHATLVFHNL
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                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U08378; NID:g473889; PIDN:AAA56668.1; PID:g473890 C;Genetics: A;Gene: APRF C;Superfamily: human signal transducer and transcription activator STAT5A
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A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator STAT5A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFNQ--AQSGNIQSTVMLDKQKELDSKVRNVKDK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 792; DB 2;
Pred. No. 1.1e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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C;Superfamily: human signal transducer and transcription activator STAT5A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAQWNQLQQLDTRYLKQLHQLYSDTFPWELRQFLAPWIESQDWAYAASKESHATLVFHNL
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No. 7.5e-14; iive 34; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 41.8%; Score 334.5; DB 2;
1 Similarity 41.4%; Pred. No. 1.5e-21;
63; Conservative 38; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVR 152
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A;Cross-references: EMBL:U18671
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A; Residues: 1-794 <LIN>
A; Cross-references: UNIPROT: P42229; EMBL: U43185; NID: g1151169; PIDN: AAB06589.1; PID: g115
C; Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mammary gland factor - mouse
N;Alternate names: stat5 protein
C;Species: Mus musculus flouse mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54772; 149273
R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A. EMBO J. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin A;Reference number: S54772; MUID:95237198; PMID:7720707
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A;Molecule type: mRNA
A;Residues: 1-793 <MUL>
A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:Z48538; NID:g758633; PIDN:CAA88
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A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved i A;Reference number: 149273; WUID:96004632; PMID:7568026
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                                                                                                                                                                                                                                                                                                                                                                                                          1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYA----ASKESHATLV
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                                                                                                                                                                                                                                                                                                                                                    14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C, Superfamily: human signal transducer and transcription activator
                                                                                                                                                                                                                                                                                  ch 23.4%; Score 187; DB 2; Length 794; 1 Similarity 31.4%; Pred. No. 1.4e-08; 48; Conservative 23; Mismatches 68; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 REANNCSSPAG----VLVDAMSOKHLOINORFEELK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.2%; Score 186; DB 2; 29.5%; Pred. No. 1.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQ 149
                                                        A,Reference number: H01043
A,Accession: G02317
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REA-----NNCSSPAGILV---DAMSOKHLO 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                Library, December 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
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Best Local Similarity 29.55
Matches 46; Conservative
     A;Lin, J:
submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-793 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: 149273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117
                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                 Matches
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-78 G.KES.
A;Cross-references: UNIPROT: P42232; UNIPROT: 09JKM1; EMBL: U21110; NID: 9747973; PIDN: AAC52
B;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
B;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
A;Reference number: S54772; MUID: 95237198; PMID: 7720707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Statuse preliminary; nucleic acid sequence not shown
A.Statuse preliminary; nucleic acid sequence not shown
A.Residues: 1-432, 'E',444-786 <MUI>
A.Residues: 1-432, 'E',444-786 <MUI>
A.Stoross-references: EMBLi248539; NID:g758635; PIDN:CAA88420.1; PID:g758636
R.Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris, EMBO J. 14, 1402-1411, 1995
A.Title: Interleukin-3 signals through multiple isoforms of Stat5.
A.Reference number: S54725; MUID:95246733; PMID:7537213
A.Actatus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                           manmary gland factor - mouse
MyAlternate names: STATS protein homolog p80
CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiDate: 02-301-1996 #sequence_revision 02-301-1996 #text_change 09-301-2004
CiAccession: I49274; S54773; S54727
CiAccession: I49274; S54773; S54727
CiAccession: I49274; S54773; S14727
CiAccession: I49274; S54773; S14727
CiAccession: I49273; MulD:96004632; PMID:7568026
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                                                                                                                                                  61 FIFTDQLNYECGRCSQDPESLLLQHNLRKFCRDIQP-FSQDPTQLAEMIFNLLEEKRIL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 FHNLLGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LEGLVQELQKKAEHQVGEDGFLLKIKLGHYATQLQSTYDRCPMELVRCIRHILYNEQRLV 120
                                                                                                                 HNLLGEIDQQYSRFLQE-SNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLL 116
1 MAMWIQAQQLQGDALHQMQALYGQHFPIEVRHYLSQWIESQAWDSIDLDNPQENIKATQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription activator stat5A - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #Sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYA----ASKESHATLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNÅ
A;Residues: 1-432,'E',434-786 <AZA>
A;Geneties:
A;Gene: Statsb
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 786;
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                                                                                                                                                                                                                                  117 QTAATAAQQGGQANHPTAAVVTEKQQ-MLEQHLQDVR 152
                                                                                                                                                                                                                                                                                     120 IQAQRAQLEQGE---PVLETPVESQQHEIESRILDLR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 QTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REANNGSSPAGS ---- LADAMSQKHLQINQTFEELR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 23.5%; Score 188; DB 2; Local Similarity 30.1%; Pred. No. 1.1e-08; Ne 47; Conservative 26; Mismatches 75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: I49274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S:
Matches 47
                                                                                                                    28
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R;Quelle, F.W.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M..; Clevel, Mol. Cell. Biol. 15, 3336-3343, 1995
Mol. Cell. Biol. 15, 3336-3343, 1995
A;Title: Cloning of murine Stat6 and human Stat6, Stat proteins that are tyrosine phosphol A;Reference number: I57557; WUID:95280934; PMID:7760829
A;Accession: 157557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P52633; GB:L47650; NID:g1008876; PIDN:AAA79006.1; PID:g100887.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Hou, J.; Schindler, U.; Henzel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
187 NL-----LDTTRKLENLTDIERQLSSRKQLQNEIPETDAEAKSAAEAKSAENQPAAAKPA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-Binding Protein and transcription factor - mouse C;Species: Was musculus (house mouse) C;Species: Way-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004 C;Accession: IS7557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LGEIDQQYSRFLQE---SNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAQWNQLQQLDTRYLKQLHQLYSDTFPWELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1848 <HOU>
A;Cross-references: UNIPROT:P42226
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: human signal transducer and transcription activator STATSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGEIDQ-----QYSRFLQESNVL---YQHN----LRRIKQFLQS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 265, 1701-1706, 1994
A;Title: An interleukin-4-induced transcription factor: IL-4 stat.
A;Reference number: A54740; MUID:94367369; PMID:8085155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 848;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 837;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-837 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.1%; Score 97; DB 2
Best Local Similarity 24.8%; Pred. No. 1.2;
Matches 29; Conservative 21; Mismatches
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Best Local Similarity
'-hes 43; Conserva
                                                              139 EKQ 141
                                                                                                                    242 ESK 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics
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                                                                                         C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accessina S55527; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corriganda. Mammary gland factor (MGF) is a novel member of the cytokine regula A;Accession: S55527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable lipoprotein YPO2915 [imported] - Yersinia pestis (strain C092)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
Cdeno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Stutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Cross-references: UNIPROT: Q8ZCQ6; GB:AL590842; PIDN: CAC92164.1; PID:g15980878; GSPDB:d
                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT: P42231; EMBL:X78428; NID:9602354; PIDN:CAA55191.1; PID:96023 A,Note: this is a revision to the sequence from reference S44353
R,Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 13, 2182-2191, 1994
A,Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcript, R,Reference number: S44353; MUID:94244619; PMID:7514531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQT---AATAAQQGGQANHPTAAVVT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 FHNLLGEIDQQYSRFLQESNVLYQHNL-RRIKQFLQSRYLEKPMEIARIVARCLWEESRL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 YSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNLLGEIDQQYSRFLQESNVLYQH 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYA----ASKESHATLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 17-716, RHLHGPGSLPSR',729,'P',731,'ASL' <WAW>
A;Cross-references: EMBL:X78428
A;Cross-references: EMBL:X78428
A;Note: this sequence has been revised in reference S55527
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 18.4%; Score 147.5; DB 2; Length 'Local Similarity 27.3%; Pred. No. 4.1e-05; hes 42; Conservative 27; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>:</u>
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121 VREATN----
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                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-794 <WAK>
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A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
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Matches 36
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A;Introns: 94/3; 124/3; 150/3; 209/3; 248/3; 311/3; 424/3; 734/2; 934/2; 1104/3; 1167/3;
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A,Cross-references: EMBL:Z92788; PIDN:CAB07214.1; GSPDB:GN00019; CESP:ZK1151.1
A,Experimental source: clone F53B8
R,Harris, B.
submitted to the EMBL Data Library, March 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA.
A;Residues: 1-1355 <MIZ>
A;Cross-references: EMBL:293398; PIDN:CAB07724.1; GSPDB:GN00019; CESP:ZK1151.1
A;Experimental source: clone ZK1151
                                                                                                                                                                                            hypothetical protein ZK1151.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T22552; T27703
R;Harris, B.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19580
A;Accession: T22552
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C; Accession: T4028 # Sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C; Accession: T4028 # A; Reference number: Z21918 # A; Reference number: Z21918 # A; Status: preliminary; translated from GB/EMBL/DDBJ # A; Status: preliminary; translated from A; Residues: 1-371 < WOOD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
133 TAAVVTEKOOMLEOHLOD 150
                                                  168 TPANGTGPSEALAMLLOE 185
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A; Accession: T27703
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A;Gene: CESP:ZK1151.1
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                                                                                                               737 QW----DWILALSKCIEEHIRDALNIKSFMEEASDA-EAWIQEQSVRIENNYNRTDFSIE 791
                                                                                      4 WNQLQQLD----TRYLKQ-LHQL-----YSD------TFPMELRQFLA 35
                                                                                                                                                                      36 PWIESQDWAYAASK--ESHA--TLVFHNLLGEIDQQYSRFLQESNVLYQHNLRRIKQFLQ 91
                                              Gaps
                                            42;
11.0%; Score 88; DB 2; Length 1355; 25.3%; Pred. No. 13; ive 25; Mismatches 57; Indels
                                                                                                                                                                                                                                                             --SRYLEKPMEIARIVARCLWEESRLLQTAATAA---QQGGQANHP 132
                                                                                                                                                                                                                                                                                        |:| : | | : | | : | | EGERFLRELDEIKEILNKYHQVI,MALTERCASISPLWQRGERIPHP 837
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hypothetical protein SPBC354.07c - fission yeast (Schizosaccharomyces pombe)
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A;Cross-references: EMBL:AL022071; PIDN:CAA17807.1; GSPDB:GN00067; SPDB:SPBC354.07c A;Experimental source: strain 972h-; cosmid c354

A;Gene: SPDB:SPBC354.07c

A; Map position: 2 A;Introns: 8/2; 75/3

10.3%; Score.82.5; DB 2; Length 371; 24.0%; Pred. No. 8.4; Query Match Best Local Similarity

6 206 G----YFRGTKNSFKATIFEKNEDPDYIVEGVWTGESKLTIPSLKSTIFFLSIPSLEAT 260 261 PITVKPESEMGDWESRNVWKE-----VSAALASGNYD-----IVSSKKSTIEQSQRDM 309 97 ----KP-MEIARIVARCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDV 151 -LRRIKOFLOSRYLE-- 96 5 NOLOOLDTRYLKOLHQLYSDTFP---MELROFLAPWIESQDWAYAASKESHATLVFHNLL 61 51; Gaps 57; Indels 31; Mismatches 62 GEIDQQYSRFLQES -- NVLYQHN-44; Conservative 152 RKR 154 **RKK 311** 309 Matches g ò 임 ò ò g à Б

C'Accession: F71884
**Ala, R.A.; Ling, L.S.L.; Mollr, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Inves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.; Nature 397, 176-180, 1999
**Affile: Genomic sequence comparison of two unrelated isolates of the human gastric path, A;Reference number: A71800; MUID:99120557; PMID:9923682 robable lipopolysaccharide biosynthesis protein - Helicobacter pylori (strain J99) C.Species: Helicobacter pylori A.Variety: strain J99 C.Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-373 <ARN>

A;Cross-references: UNIPROT:Q9ZKW4; GB:AE001511; GB:AE001439; NID:g4155382; PIDN:AAD0639 A;Experimental source: strain J99

A;Gene: jhp0820

26; Indels 13; Gaps Query Match 10.3%; Score 82.5; DB 2; Length 373; Best Local Similarity 33.8%; Pred. No. 8.4; Matches 27; Conservative 14; Mismatches 26; Indels 13

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18 LHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNLLGEIDQQYSRFLQESNV 77

LYQHNLRRIKQFLQSRYLEK 97 78 334 LNDHNKKSFFEFLNTRLNKK 353

Search completed: May 5, 2005, 15:01:50 Job time : 18.2329 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

5, 2005, 14:55:35 ; Search time 41.6706 Seconds (without alignments) 1892.467 Million cell updates/sec May

US-10-090-185-8 800 1 MAQWNQLQQLDTRYLKQLHQ......AVVTEKQQMLEQHLQDVRKR 154 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P40763 homo sapien	P42227 mus musculu	P52631 rattus norv	P61635 bos taurus	Q6dv79 gallus gall	Q9pvx8 xenopus lae	Q7zxk3 xenopus lae	Q7zts5 brachydanio	Q6nv46 brachydanio	093599 brachydanio				Q90y16 tetraodon f	Q8jgn0 xenopus lae		Q68d00 homo sapien	_	Q7tp57 rattus norv	Q99k94 mus musculu	P42225 mus musculu	Q8c3v4 mus musculu	Q8c497 mus musculu	Q9d323 mus musculu	Q9qxk0 rattus norv	Q8c8m3 mus musculu	Q764m5 sus scrofa		013132 oncorhynchu	013131 oncorhynchu	Q801y2 carassius a
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ID	STA3 HUMAN	STA3 MOUSE	STA3 RAT	STA3 BOVI	Q6DV79	Q9PVX8	Q7ZXK3	Q7ZTS5	Q6NV46	093599	013133	Q6DVF3	O6GUE7	Q90Y16	Q8JGN0	STA1_HUMAN	Q68D00	Q6P6Q7	Q7TP57	Q99K94	STA1_MOUSE	Q8C3 <u>V</u> 4	Q8C497	Q9D323	Q9QXK0	QBCBM3	Q764M5	Q90Y17	013132	013131	Q801Y2
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% Query Match Length	770	770	770	770	771	769	992	414	786	908	767	765	785	764	751	750	750	712	1165	712	749	749	749	749	749	755	757	758	754	754	718
% Query Match	99.0	99.0	0.66	98.2	97.4	95.0	93.6	86.8	86.8	86.8	86.4	85.7	85.7	85.2	50.1	47.5	47.5	47.4	47.4	47.2	47.2	47.2	47.2	47.2	47.2	47.2	47.2	44.3	43.9	43.2	42.1
Score	792	792	792	786	779	760	749	694.5	694.5	694.5	691.5	685.5	685.5	681.5	401	380	380	379	379	378	378	378	378	378	378	378	378	354.5	351	346	336.5
Result No.		7	n	4	2	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

093598 brachydanio (06p943 brachydanio P42228 mus musculu (14765 homo sapien (06bb2 rattus norv (72x77 brachydanio (98w24 brachydanio (72x53 brachydanio (801x2 brachydanio (801y2 brachydanio (801y2) brachydanio (800y1) brachydanio (800y1)
093598 QCE943 QCE943 STA4_MOUSE STA4_HUMAN QCEHEZ QCENZ77 QBAWZ QCZZ77 QBAWZ QCZZ3 QBOJU9 QBOFUB QBAWZ QGOFUB
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ALIGNMENTS

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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I. Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coactivator NCOA/SRCIa.";
J. Biol. Chem. 277:8004-8011(2002).
-!- FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various acute-phase protein genes.
-!- PATHWAY: Involved in the gpl30-mediated signaling pathway.
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOAI.
-!- SUBCELLUJAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.
                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION ON SERINE.
MEDLINE=95215843; PubMed=7701321;
Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
"Requirement of serine phosphorylation for formation of STAT-promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOJG-P40761-2; Sequence-VSP 010474;
ISOJG-P40765-2; Sequence-VSP 010474;
IISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas.

PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, ILF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STRT3 homodimers and maximal transcriptional activity.

SIMILARITY: Belongs to the transcription factor STAT family.

SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11773079; DOI=10.1074/jbc.M111486200;
Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
"Functional interaction of STAT3 transcription factor with the
                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                             Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P40763-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AJ012463, CAA10032.1; --
EMBL, AJ012463, CAA10032.1; --
EMBL, AY572796, AAS66986.1; --
EMBL, BC00627, AAH00627.1; --
EMBL, BC014482, AAH4482.1; --
                                                                                                                                                                                                  SEQUENCE OF 564-704 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       Science 267:1990-1994 (1995)
                                                                                                                                   and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGNC:11364; STAT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H-InvDB; HIX0013840; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERACTION WITH NCOAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A54444; A54444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFAC; T01493;
                                                                                                                                                                                                                         rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                     complexes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
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. ARARAR TRANSPORTATION OF THE TRANSPORTATIO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
                                                                         .; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BALB/C; TISSUE=Liver;
MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;.
Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
Yoshida K., Sudo T., Naruto M., Kishimoto T.;
"Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
related transcription factor involved in the gp130-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
AND 632-640.
                                                                                                                                                                                                                                                                                                                                                                                                           Phosphotyrosine (by JAK) (By similarity)
                                                                                                                                                                                                                                                                                                                                    Activator; Alternative splicing; DNA-binding; Nuclear protein;
Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
DOMAIN S80 670 SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
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0
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01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last amnotation update)
Signal transducer and activator of transcription 3 (Acute-phase
  Fitranscription factor activity; TAS.
P:cell motility; TAS.
P:JAK-STAT cascade; TAS.
P:negative regulation of transcription from P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphoserine (By similarity)
Missing (in isoform Del-701)
/FTIG=VSP_010474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q -> K (in dbsNP:1803125).
/FTId=VAR_018683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6C00632211C8012D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q -> H (in Ref. 1)
P -> S (in Ref. 1)
K -> N (in Ref. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 792; DB 1;
Pred. No. 7.3e-60;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F -> Y (in Ref. 1)
V -> L (in Ref. 1)
T -> A (in Ref. 1)
GO; GO:0003700; F:transcription factor activit GO; GO:0006928; P:cell motility; TAS. GO; GO:000729; P:GAK-STAT cascade; TAS. GO; GO:0000122; P:negative regulation of trans GO; GO:0007399; P:neurogenesis; TAS. GO; GO:0007189; P:neurogenesis; TAS. InterPro; IPR009867; PS3_like_DNA_bnd. InterPro; IPR00980; SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VAR 018679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88067 MW;
                                                                                                                                                                                                             Pfam; PF0017; ST2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF0264; STAT bind; 1.
Pfam; PF02865; STAT bint; 1.
PROSITE; PS50001; SF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.7
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                           705
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460
548
561
667
730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143
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730
770 AA;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Riausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenco L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L.,

B Diatcheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Dosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Red Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                   MEDLINE=95014185; PubMed=7523373;
Raz R., Durbin J.E., Levy D.E.;
"Acute phase response factor and additional members of the interferonstimulated gene factor 3 family integrate diverse signals from cytokines, interferons, and growth factors.";
J. Biol. Chem. 269:24391-24395(1994).
                                                                               Zhong Z., Wen Z., Darnell J.E. Jr.,
"Steats: a STAT family member activated by tyrosine phosphorylation in response to epidermal growth factor and interleukin-6.";
science 264:95-98(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.
MEDLINE-5934205; Pubmed=7543024; DOI=10.1016/0092-8674(95)90311-9;
WHEN Z., Zhong Z., Darnell J.E. L. "Maximal activation of transcription by Stat1 and Stat3 requires both
                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11161808; DOI=10.1006/geno.2000.6433;
Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T.,
Dewar K., Hennighausen L.;
"Structure of the mouse stat 3/5 locus: evolution from Drosophila to
                                                                                                                                                                                                                                                                                                                                  Schaefer T.S., Sanders L.K., Nathans D.; "Cooperative transcriptional activity of Jun and Stat3 beta, a short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CS7BL/6J, and NOD/LtJ;
Davoodi.Semiromi A., She J.-X.;
"A mutant Stat5b with weaker DNA binding defines a key defective pathway in non-obese diabetic (NOD) mice.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM STAT3B).
STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
MEDLINE=96016116; Pubmed=7568080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine and serine phosphorylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM STAT3A).
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                                          SEQUENCE FROM N.A. (ISOFORM STAT3A)
                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM STAT3A)
                                                             TISSUE=1119mus;
MEDLINE=94188718; PubMed=8140422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 71:150-155(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.
 pathway.";
Cell 77:63-71(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zebrafish to mouse."
                                                                                                                                                                                                                                                                                                                                                                 Stat3.";
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=129/SvJ;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                             -i-FUNCTION: Transcription factor that binds to the interleukin-6
-i-FUNCTION: Transcription factor that binds to the interleukin-6
-i-FUNCTION: Transcription genes. STAT3B interacts with the N-terminal acute-phase protein genes. STAT3B interacts with the N-terminal part of JUN to activate such promoters in a cooperative way.
-i-PATHWAY: Involved in the gpl30-mediated signaling pathway.
-i-SUBCUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).
-i-SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name-Del-701;
Isole P42227-3; Sequence=VSP 010475;
Isole P42227-3; Sequence=VSP 010475;
Isole P42227-3; Sequence=VSP 010475;
Isole P42227-3; Sequence=VSP 010475;
Isole PABCIFICITY: STAT3A is seen in the liver, although in a much less abundant manner.
Isole Babindant manner.
Isole Babindant manner.
Isole PABCIFICITY: STAT3A isole Babindang Stata is important for the formation of stable DNA-binding STAT3 homodymes and maximal transcriptional activity (By similarity).
Isole Babindan STAT3 belongs to the transcriptional activity (By similarity).
Isole Babindan STAT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0005634; C:plasma membrane; IDA.
GO; GO:0003677; F:DNA binding; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0005515; P:transcriptional activator activity; IDA.
GO; GO:0007259; P:Transcriptional activator activity; IDA.
GO; GO:0006357; P:transcription of transcription from Pol II pro...
InterPro; IPR000867; PS3_like_DNA_bnd.
InterPro; IPR001217; STAT.
X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;
Becker S., Groner B., Mueller C.W.;
"Three-dimensional structure of the Stat3beta homodimer bound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3D-structure, Activator, Acute phase, Alternative splicing, Direct protein sequencing, DNA-binding, Nuclear protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P42227-2; Sequence=VSP_006287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in response to phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, U06922; AAA19452.1; --
EMBL, U08378; AAA56668.1; --
EMBL, U30709; AAC52612.1; --
EMBL, AF29489; AAL59017.1; --
EMBL, AY29489; AAC75418.1; --
EMBL, AY29490; AAG75419.1; --
EMBL, BC003806; AAH03806.1; --
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Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT_int; 1.
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PDB; 1BG1; X-ray; A=1-722.
TRANSFAC; T01574; -.
MGD; MGI:103038; Stat3.
                                                                                                                                                                                                              Nature 394:145-151(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Stat3A;
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Biol. Chem. 270:29998-30006(1995)
                                                                                                                                                                                                                                                                                                                            MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                   1 MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
                Phosphotyrosine (by JAK) (By similarity).
                                 TTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Transcription factors Stat3 and Stat5b are present in rat liver nuclei late in an acute phase response and bind interleukin-6 response
                                                                                                                                                                                                                                                                                                                    MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                        FDMDLTSECATSPM -> FIDAVWK (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998; Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F., Fey G.H.;
                                                                                                                                                                                                                                                                                                     ö
                                                                                  S->A: Decreased transcriptional
                                                                                                                                                                                                                                                                                   Length 770;
                                                               Missing (In isoform Del-701). /FTId=VSP_010475.
                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                E -> K (in Ref. 2).
S -> T (in Ref. 2 and 4).
M -> I (in Ref. 1).
Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
02-0CT-2094 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                                  Score 792; DB 1;
Pred. No. 7.3e-60;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                      TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                         FTId=VSP 006287
                                                                                                                                                                                                                                                                                                                                                                                                                                               770 AA.
                                                                                          activation.
                                                                                                                                                                                                                                                                                                                             =
SH2 domain;
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.7
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
               705
727
770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Liver;
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Phosphorylation;
        580
705
727
716
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              MOD_RES
MOD_RES
VARSPLIC
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HELIX
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                    acute-phase protein genes.
-!- PATHWAY: Involved in the gp130-mediated signaling pathway.
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOAI (By similarity).
-!- SUBCELULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation (By similarity).
-!- FTM: Tyrosine phosphorylation (By similarity).
-!- FTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, ILF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity (By similarity).
-!- SIMILARITY: Belongs to the transcription factor STAT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
-!- FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF0017; STAT_alpha; 1.
Pfam; PF01864; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
Pfam; PF02871; SH2; 1.
PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     705 705 Phosphotyrosine (by JAK) (By similarity) 727 727 Phosphoserine (By similarity). 770 AA; 88039 MW; D74AQC76954754ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-0CT-2004 (Rel. 44, Last sequence update)
Signal transducer and activator of transcription 3.
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HSSP, P42227; 1BG1.
RGD, 3772; Stats.
InterPro; IPR00980; F53_like_DNA_bnd.
InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
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P61635;
O5-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last seq.
25-OCT-2004 (Rel. 45, Last anno
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us-10-090-185-8.rup

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TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=stat 3;
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             embryos independent of BMP-4.";
Dev. B101. 1216-481-490(1999).
EMBL; ABO17701; BAA86061.1; --
HSSP; P42227; IBG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
SMART; SW00255; STAT_int; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                    Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                    Best Local Similarity 96.8
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                  PROSITE, PS50001; SH2
SEQUENCE 771 AA; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Matches 145;
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                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                   TISSUE-Mammary gland;

A Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
The STATSB-encoding gene was flipped across the STAT3/STAT5A-locus
The STATSB-encoding gene was flipped across the STAT3/STAT5A-locus
The STATSB-encoding Gene was flipped across to the interleukin-6

I. Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

I. Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

I. FUNCTION: Transcription factor that binds to the interleukin-6

I. Submitted (JAN-2004) in the gpl30-mediated signaling pathway.

I. PATHWAY: Involved in the gpl30-mediated signaling pathway.

I. SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).

I. SUBCELULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation (By similarity).

I. SIMILARITY: Belongs to the transcription factor STAT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LGEIDOOYSRFLOESNVLYOHNLRRIKOFLOSRYLEKPMEIARIVARCLWEESRLLOTAA 120
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation 3.
Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
Archosauria, Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhou G.Y., Leung F.C.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, 944641397, A47646897.1; -..
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
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Pred. No. 2.4e-59;
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727 727 PP
770 AA; 87974 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007402; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; P53_like_DNA_bnd.
InterPro; IPR00980; STAT.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008967; P53_like_DNA_bnd.
InterPro; IPR00890; SH2.
InterPro; IPR00171; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 771;
                                                                                                                                                                                                                                                                                                                                                                     97.4%; Score 779; DB 2; Length 77; 96.8%; Pred. No. 9.7e-59; wismarches 2; Indels
                                                                                                                                                                                                                                                                                                                                        771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50001; SH2; 1.
769 AA; 87974 MW; 0905C03263303069 CRC64;
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Last annotation update)
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Name=stat3;
                         InterPro;
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                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7ZTS5
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninol P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Makealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
M. Jones S.J., Marra M.A.,
M. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                  MAQWINQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
                                                MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAFAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0005634; Cincleus; IEA.
GO:0004871; F:signal transducer activity; IEA.
GO:0004870; F:transcription factor activity; IEA.
GO:0007242; P:intracellular signaling cascade; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopos laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUBE-Embryo;
MEDLINE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Embryo;
Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                           TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                      766 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC044717; AA444717.1; HSSP; P42227; 1BG1.
GO; GO:0005634; C:nucleus; IEG GO; GO:0004871; F:signal tran GO; GO:0003700; F:transcriptic GO; GO:000742; P:intracellul GO; GO:000325; P:regulation
                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus,
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=stat3-A;
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                                                                                                                                                                                                                                                                                                                                                                                      Q7ZXK3
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Q7ZXK3
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CARAIN-AB; TISSUE-Whole body;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METARUSPERS R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Maltachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J. Usdin T.B., Roanddo M.F., Casavant T.L., Scheetz T.E.,

Raha S.B., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roard S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Raywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

M. Jones S.J., Marray M.A., Soney M.A., Peters S., Schein J.E.,

M. Jones S.J., Marray M.A., Schein S.D., Charather M., Bouffard S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

M. Jones S.J., Marray M.A., Soney M.A., Peter M.A., Schein J.E.,

M. Jones S.J., Marray M.A., Smallus D.E., Schnerch A., Schein J.E.,

M. Jones S.J., Marray M.A., Schein J.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSTYLEKPMEIARIVARCLWEEGRLLQTAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAFAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                           87599 MW; 31018A3321CCEB9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                        93.6%; Score 749; DB 2; L
92.2%; Pred. No. 3.7e-56;
iive 6; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 AA
P53 like DNA bnd.
                                                                                                         Pfam; PF00017; SHZ; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT bind; 1.
SMART; SMO0252; SHZ; 1.
SMOXTE; PS50001; SHZ; 1.
SEQUENCE 766 AA; 87599 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=AB; TISSUE=Whole body; Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                    IPR000980;
IPR001217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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NCBI_TaxID=7955;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oates A.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAQWNQLQQLETRYLEQLYHLYSDSFPMELRQFLAPWIESQDWAYAANKESHATLVFHNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
                          GO; GO:0005634; C:nucleus; IEA.

GO; GO:0004871; F:signal transducer activity; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:000555; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR00967; P33 like_DNA_bnd.
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                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Indels
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Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                         Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
SEQUENCE 414 AA; 48253 MW; OFFD1B509B7526BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.8%; Score 694.5; DB 2
86.4%; Pred. No. 9.3e-52;
iive 10; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 86.49
Matches 133; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyprinidae; Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stat3 protein.
Name=stat3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monse
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ZFIN;
GO; GC
GO; GC
GO; GC
GO; GC
GO; GC
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Q6NV46
  LID DTT TO DTT T
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LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
ZFIN; ZDB-GENE-980526-68; stat3.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007407; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; P53_like_DNA_bnd.
InterPro; IPR001217; STAT.
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GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004871; F:signal transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008967; P53_like_DNA_bnd.
InterPro; IPR00980; STAT.
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 786;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                             786 AA; 90039 MW; FC7371D0B0E5447E CRC64;
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92151 MW; 74BC4EA401C3C942 CRC64;
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EMBL; AJ005693; CAA06677.1; -.
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                          86.8%; Score 694.5; DB 2;
86.4%; Pred. No. 2e-51;
live 10; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                                                                                                                                               Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
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Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
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08,
26,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 86.48
Matches 133; Conservative
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01-NOV-1998 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                   SHZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyprinidae; Danio.
NCBI_TaxID=7955;
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PROSITE; PS50001;
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06GUE7;
05-JUL-2004
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Q6GUE7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                         LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                 1 MAQWNQLQQLETRYLEQLYHLYSDSFPMELRQFLAPWIESQDWAYAANKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQUENCE FROM N.A.

A Johnson M.C., Mourich D.V., Leong J.C.;
Length Led (Jun-1996) to the EMBL/GenBank/DDBJ databases.

R MSP; P42227; 1BG1.
R GO; GO:0006874; F:signal transducer activity; IEA.
R GO; GO:0003700; F:transcription factor activity; IEA.
R GO; GO:0007242; P:intracellular signaling cascade; IEA.
R GO; GO:0007285; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009967; P53 like_DNA_bnd.
InterPro; IPR001997; STAT.
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                                           MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
Gaps
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Actinopterygii, Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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    1;
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85.7%; Pred. No. 3.4e-51;
live 12; Mismatches 9; Indels 1.
  10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY; .
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  Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=rbtStat3;
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25-OCT-2004
25-OCT-2004
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Q6DVF3;
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Q6DVF3
ID Q6DVF
AC Q6DVF
DT 25-OC
DT 25-OC
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61 LGEIDQQYSRFLQENNVLYQHNLRRIKQHLQSKYLEKPMEIARIVARCLWEEQRLLQT-A 119
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Ray, 2000, 11. -...

Roy, 60:0000534; C:nucleus; IEA.

Roy, 60:0000717; F:stanscription factor activity; IEA.

Roy, 60:00007242; P:intracellular signaling cascade; IEA.

Roy, 60:00007285; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR00980; SH2.

R InterPro; IPR001217; STAT.

R Pfam; PF00177; STAT.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
07-Zias latipes (Medaka fish) (Japanese ricefish).
07-Zias Jachendoni, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Adanthopoterygii, Percomorpha, Atherinomorpha;
07-Zias Adrianichthyidae, Oryzias.
Signal transducer and activation of transcription factor 3. Oryzias latipes (Medaka fish) (Japanese ricefish). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii, Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AY639947; AAT64912.1; -...
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:000742; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; PS3_like_DNA_bnd.
InterPro; IPR00980; SH2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                            Liu R., Hong Y.; Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87566 MW; FSD01408748EC703 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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85.7%; Score 685.5; DB 2
Best Local Similarity 85.1%; Pred. No. 1.1e-50;
Matches 131; Conservative 11; Mismatches 11
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Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
PROSITE; PS50001; SH2; 1.
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                                                                                                                                                               LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                               61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LGEIDQQYSRFLQESNVLYQHNLRRIKQHLQSKYLEKPMEIARIVARCLWEEQRLLQTAS 120
                                                                                                                            1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAQWNQLQQLETRYLEQLYHLYSDSFPMELRQFLAPWIESQDWAYAANKESHATLVSHNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF307106; AAL09415.1; -...
HSSP; P42227; 1BG1.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006555; P:regulation of transcription, DNA-dependent; IEA.
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                                                              DB 2; Length 785;
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                                                                                       11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307106; AAL09415.1; -.
                                      89643 MW; 81F231BDE27DE938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; 1.
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                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                120 TSTSQDGSAAHPTGTVVTEKOOILEHNLODIRKR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.7%; Score 685.5; DB 2
85.1%; Pred. No. 1.2e-50;
ive 11; Mismatches 11
                                                                                                                                                                                                                 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                                                                                                                                                                                                                                                                                                Fetraodon fluviatilis (Puffer fish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
SWART; SM00252; SH2; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
PROSITE; PS50001; SH2; 1.
                                                                        Best Local Similarity 85.1.
Matches 131; Conservative
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                                    785 AA;
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PROSITE;
SEQUENCE
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                                      SEQUENCE
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                                                              Query Match
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21098508; PubMed=11164887; DOI=10.1016/S0145-305X(00)00050-1; Turpen J.B., Carlson D.L., Hunng C., "Cloning and developmental expression of Xenopus Statl."; Dev. Comp. Immunol. 25:219-229(2001).
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GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transecription factor activity; IEB.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000967; F3] like_DNA_bnd.
InterPro; IPR000980; SH2.
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                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleost
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.1%; Score 401; DB 2; Length 751; Best Local Similarity 48.7%; Pred. No. 4e-26; Matches 75; Conservative 33; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Turpen J.B., Carlson D.L., Huang C.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY101602; AAM51552.1; -.
HSSP; P42224; 1BF5.
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86497 MW; 788810A08B0889EA CRC64;
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Last annotation update)
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751 AA
                                                           Created)
                                                                                                                                                                            Xenopus laevis (African clawed frog)
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Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
SMART; SM00252; SH2; 1.
                                                     01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
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PROSITE; PS50001;
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Search completed: May 5, 2005, 14:57:40 Job time : 43.6706 secs

RESULT 15

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1290
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1 RCHWEESRLLQTAATAAQQG......LNYQLKIKVCIDKDSGDVAA 271
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                               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB seq
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Description	Sequence 9, Appli	Sequence 12, Appl	Sequence 12, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 8, Appli	Sequence 56, Appl	Sequence 2, Appli	Sequence 780, App	Sequence 780, App	~	Sequence 349, App
SUMMARIES ID	US-10-090-185-9	US-09-876-773-12	US-10-639-617-12	US-10-380-020-4	US-10-380-020-2	US-10-380-020-5	US-10-045-792-8	US-10-038-010-56	US-10-117-087-2	US-09-925-302-780	US-09-925-302-780	US-10-116-275-329	US-10-116-275-349
DB	13	11	11	15	15	15	14	14	14	σ	10	15	15
% Query Match Length DB	271	770	770	720	769	169	770	770	770	793	793	770	770
* Query Match	100.0	100.0	100.0	99.2	99.2	99.2	99.2	99.5	99.5	99.2	99.2	0.66	98.8
Score	1388	1388	1388	1377	1377	1377	1377	1377	1377	1377	1377	1374	1372
Result No.		~	٣	4	S	9	7	80	6	10	11	12	13

US-10-090-185-14 Sequence 14, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 28, Appl Sequence 21, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 23, Appl Sequence 23, Appl Sequence 24, Appl Sequence 27, Appl Seque	ALIGNMENTS .0090185 .77a1 Melissa H fines E FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR 1 CTIONS .US/10/090,185 .03-04 .03-04 .03-04 .03-04	100.0%; Score 1388; DB 13; Length 271; ; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKWKVVE 60
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2523 2223 2223 2223 2223 2223 2223 2223	ion US/100901 020197647A1 iaokui xynska, Melia xynska, Melia Jr., James I METHODS FOR INTERACTION 1-1-253 NUMBER: US/1 2002-03-0; UMBER: 09/38* 1999-08-31 S: 43 Ver. 2.0	10 10 10 10 10 10 10 10 10 10 10 10 10 1
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	SULT 1 Sequence 9, Application US/1 Publication No. US2002019764 GENERAL INFORMATION: APPLICANT: Zhang, Xiaokui APPLICANT: APPLICANT: Wrzeszczynska, APPLICANT: Wrzeszczynska, APPLICANT: Wrzeszczynska, APPLICANT: Wrzeszczynska, APPLICANT: Wrzeszczynska, TITLE OF INVENTION: METHODS TITLE OF INVENTION: METHODS TITLE OF INVENTION: INTERA TITLE OF INVENTION: METHODS TITLE OF INVENTION: METHODS TITLE OF INVENTION WIMBER: CURRENT APPLICATION NUMBER: OF RIGHT OF SEQ ID NOS: 43 SOFTWARE: PATENTING DATE: 1999-08- NUMBER OF SEQ ID NOS: 43 SOFTWARE: PATENTING VET: 2.0 EMORTH: 271 TYPE: PRT ORGANISM: MUS MUSCULUS	100.0%; Conservative 0; CumEESRLLQTAATAAQQGG
11299 111102 111102 111162 111165 111165 111165 111165 1165 1165	SULT 1 SULT 1 Sequence 9, As Publication N GENERAL INFORM APPLICANT: 21 APPLICANT: 21 APPLICANT: 1 APPLICANT:	tch 271 1 1 61
4 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RESULT 1 US-10-090-185-9 Sequence 9, Application US/1009(Sequence 9, Application US/1009(Publication No. US20020197647A1) APPLICANT: Wrzeszcynska, Mel. APPLICANT: Horvath, Curt M APPLICANT: Horvath, Curt M APPLICANT: Darnell Jr., James ITILE OF INVENTION: METHODS FOI TITLE OF INVENTION: METHODS FOI TITLE OF INVENTION: METHODS FOI TITLE OF INVENTION: METHODS FOI FILE REPERENCE: 600-1-253 CURRENT APPLICATION NUMBER: US, CURRENT APPLICATION NUMBER: US, NUMBER OF SEQ ID NOS: 43 SEQ ID NO 9 LENGHYH: 271 TYPE: PRT CREANISM: MUS musculus US-10-090-185-9	Query Ma Best Loc Matches Qy Db Db

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287 LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
                                                    107 RCLWEBSRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKWKVVE 166
                                                                                                    61 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
                                                                                                                                   121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
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FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                            347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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APPLICATION NUMBER: US/10/639,617
FILING DATE: 12-Aug-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Darnell Jr., James E. Schindler, Christian W. Fu, Xian-Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-639-617-12; Sequence 12, Application US/10639617; Publication No. US20050079543A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 201 487-5800
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TELEX: 133521
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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AMEYVOKTLIDBELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
                                                                                                                                 LOOKVSYKGDPIVOHRPMLEERIVELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFT 240
                                                                                          LOOKVSYKGDPIVOHRPMLEERIVELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFT
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Best Local Similarity 100.0%; Pred. No. 1e-109;
Matches 271; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/984,296
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,589
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAMME: JACKSON ESQ., David A.
REFERRANCE/DOCKET NUMBER: 26,742
REFERRANCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                241 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
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APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                      RESULA 12
US-09-876-773-12
i Sequence 12, Application US/09876773
i Publication No. US20040058318A1
i GENERAL INFORMATION:
i APPLICANT: Darnell Jr., James E.
i Schindler, Christian W.
i Wen, Zilong
Zhong, Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12
                                                                                                                                                                                   TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION TELEPHONE: 201 487-5800
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 201 343-1684
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APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Pardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: 40/210/380,020
CURRENT PILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
LENGTH: 769
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APPLICANT: Pardoll, Drew
APPLICANT: Pardoll, Drew
APPLICANT: Pardoll, Drew
APPLICANT: Pardoll, Drew
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
CURRENT APPLICATION NUMBER: US/10/380,020
CURRENT APPLICATION NUMBER: US/203-03-07
PRIOR PILLING DATE: 2003-03-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.0
SEQ ID NO S.
LENGTH: 769
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Pred. No. 9.1e-109;
1; Mismatches 1;
                             TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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; Publication No. US20040052762A1
; GENERAL INFORMATION:
                                                                                                                                                                                        Sequence 2, Application US/10380020; Publication No. US20040052762A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.3%;
Matches 269; Conservative
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Publication No. US20040052762A1

GENERAL INFORMATION:

APPLICANT: Vu Hua

APPLICANT: Pardoll, Drew

APPLICANT: Dalton, William

TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof

FILE REFERENCE: 10873-009-999

CURRENT APPLICATION NUMBER: US/10/380,020

CURRENT PILING DATE: 2003-03-07

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 3.0

LENGTH: 720
                                                                                                                                                                                                                                                                          107 RCLWEESKLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE 166
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                                                                                                                                                                                          0; Indels
                                                                                                                                       100.0%; Score 1388; DB 17;
100.0%; Pred. No. 1e-109;
Live 0; Mismatches 0;
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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Best Local Similarity 100.
Matches 271; Conservative
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ORGANISM: Homo Sapiens
                                                                                              US-10-639-617-12
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                                                                                                                                                                                                                                                                                          61 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS; APPLICANT: Pierre, Legrain; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells; TITLE OF INVENTION Protein-protein interactions in adipocyte cells; CURRENT FILING DATE: 2002-07-23; PRIOR PAPLICATION NUMBER: US/10/038,010; CURRENT FILING DATE: 2001-01-02; NUMBER OF SEQ ID NOS: 67; SOFTWARE: Patentin version 3.1; Seq ID NO 56; LENGTH: 770
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                                                                                                                     Score 1377; DB 14;
Pred. No. 9.1e-109;
1; Mismatches 1;
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OTHER INFORMATION:
                                                       SEQUENCE DESCRIPTION: SEQ ID NO: US-10-045-792-8
                                                                                                                         Query Match
Best Local Similarity 99.3%;
Matches 269; Conservative
                   MOLECULE TYPE: protein HYPOTHETICAL: NO
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Matches 269; Conservative
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US-10-038-010-56
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Darnell, Jr., James E.
Kuriyan, John
TITLE OF INVENTION: A CHYSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF
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                                                                                        Length 769;
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS. CALAUDER & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                   Score 1377; DB 15;
Pred. No. 9.1e-109;
1; Mismatches 1;
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NAME: Jackson Eq., David A.
REGISTRATION NUMBER: 26, 742
REFERENCE/DOCKET NUMBER: 600-1-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-Oct-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/012,710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/10045792; Publication No. US20030003563A1. GENERAL INFORMATION: APPLICANT: Vinkemeier, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 770 amino acids TYPE: amino acid
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                                                                                   Query Match
Best Local Similarity 99.3%;
Matches 269; Conservative
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COUNTRY: USA
ZIP: 07601
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-5
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US-10-045-792-8
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TILB REPERBYCE: PROJUCATION:

APPLICANT: Rosen et al.

TILB CP INVENTION:

TILB CP INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REPERBYCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-10

PRIOR FILING DATE: 1909-03-12

NUMBER OF SEQ ID NOS: 896

SOFTWARE: PATENTION OFFE: 2.00

SEQ ID NOS: 896

SEQ ID NO 780

LENGTH: 793
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Pred. No. 9.4e-109;
1; Mismatches 1;
                                                       Query Match
99.2%; Score 1377; DB 9;
Best Local Similarity 99.3%; Pred. No. 9.4e-109;
Matches 269; Conservative 1; Mismatches 1;
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Best Local Similarity 99.3
Matches 269; Conservative
   ; ORGANISM: Homo sapiens
US-09-925-302-780
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US-09-925-302-780
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; Sequence 780, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: ROSen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARR: PatentIn Ver: 2.0
; SEQ ID NO 780
; LENGTH: 793
; TYPE: PRT
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Publication No. US20030166854A1

GENERAL INFORMATION:

APPLICANT: SERLUPI-CRESCENZI, Ottaviano

TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3

FILE REFERENCE: SERLUPI=2:

CURRENT APPLICATION NUMBER: US/10/117,087

CURRENT FILING DATE: 2002-04-08

PRIOR FILING DATE: 2000-03-19

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PATCHIN VESSION 3.0
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Pred. No. 9.1e-109;
1; Mismatches 1;
                                                   347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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Best Local Similarity
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ORGANISM: Human
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LENGTH: 770
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Sequence 14, Application US/10090185

Sequence 14, Application US/10090185

Publication No. US20020197647A1

GENERAL INFORMATION.

APPLICANT: Application Mo. US2020197647A1

APPLICANT: Areaczynska, Melissa H

APPLICANT: Horvath, Curt M

APPLICANT: Horvath, Curt M

APPLICANT: Darnell Jr., James E

TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR PI:

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION NUMBER: US/10/090,185

CURRENT FILING DATE: 2002-03-04

PRIOR APPLICATION NUMBER: 09/387,418

PRIOR APPLICATION NUMBER: 09/387,418

PRIOR PELING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 14
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                                   Length 770;
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                                   Score 1372; DB 15;
Pred. No. 2.4e-108;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                      Query Match
Best Local Similarity 98.9%;
Matchés 268; Conservative
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CRGANISM: Mus musculus
US-10-090-185-14
US-10-116-275-349
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Publication No. US20030211476A1

General InfoRMATION:

APPLICANT Elan Pharmaceutical Technology

APPLICANT: Braden, David

APPLICANT: Braden, David

APPLICANT: Braden, David

APPLICANT: Higgins, Lisa

TITLE OF INVENTION: Generatic Analysis of Peyer's Patches and Methods and

TITLE OF INVENTION: Compositions Targeting Peyer's Patches and Methods and

TITLE OF INVENTION: US/10/116,275

CURRENT FILING DATE: 2002-10-04

NUMBER OF SEQ ID NOS: 349

SEQ ID NOS: 349

SEQ ID NO 349

LENGTH: 770
                                                                Sequence 329, Application US/10116275

Publication No. US20030211476A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Lisa
TITLE OF INVENTION: Cenetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: E1067/20087
CURRENT APPLICATION WUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: Patentin version 3.1
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Best Local Similarity 98.9
Matches 268; Conservative
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ORGANISM: Homo sapiens
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US-10-116-275-349
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; ORGANISM: Rat
US-10-116-275-329
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LENGTH: 770
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241 TKVRLLVKFPEL 252

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RESULT 15

US-10-090-185-15

Squence 15, Application US/10090185

Publication No. US20020197647A1

GENERAL INFORMATION:

APPLICANT: Chang, Xiaokui

APPLICANT: Horvath, Curt M

APPLICANT: Darnell JT., James E

TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR FILE REFERENCE: 600-1-253

FILE REFERENCE: 600-1-253

CURRENT FILING DATE: 1099-08-31

PRIOR APPLICATION NUMBER: 09/387,418

PRIOR PILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 15

LENGTH: 236
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                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Mus musculus
US-10-090-185-15
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Search completed: May 5, 2005, 15:17:41 Job time : 115.139 secs THIS PAGE BLANK (USPTO)

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1 RCLWEESRLLQTAATAAQQG.......LNYQLKIKVCIDKDSGDVAA 271
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-852-091-12
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US-09-364-970-3
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US-09-317-185-12
US-08-212-185-12
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US-09-117-087-2
US-09-117-087-2
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28 1168 84.1 229 3 31 1155 81.2 229 3 31 1145 81.1 229 3 31 1145 81.2 229 3 31 1142 81.2 229 3 31 1142 81.2 229 3 31 1143 32 229 3 34 67.9 185 3 36 669 48.2 129 3 36 669 48.2 129 3 37 653 12 143 3 39 647 46.6 712 1 40 647 46.6 712 2 41 647 46.6 712 3 42 647 46.6 712 3 42 647 46.6 712 3 42 647 46.6 712 3 43 647 46.6 712 3 44 647 46.6 712 3 45 647 46.6 712 3 46 647 46.6 712 3 47 46.6 712 3 48 647 46.6 712 3 48 647 46.6 712 3 49 647 46.6 712 3 41 647 46.6 712 3 42 647 46.6 712 3 43 647 46.6 712 3 44 647 46.6 712 3 45 647 46.6 712 3 46 647 46.6 712 3 47 46.6 712 3 48 647 46.6 712 3 48 647 46.6 712 3 48 647 46.6 712 3 48 647 46.6 712 3 48 647 46.6 712 3 48 647 46.6 712 3 49 647 46.6 712 3 49 647 46.6 712 3 40 647 46.6 712 3 41 11		IGNMENT H ENTIFYI) 87,418A	ore 1388; #ismatches #HHANDERTER #HIT
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		ESULT 1 S-09-387-418A Sequence 9, Patent No. 6 GENERAL INFO APPLICANT: APPLICANT: APPLICANT: TITLE OF IN FILE REFERE CURRENT APPLICANT: NUMBER OF SOFTWARE: SEQ ID NO 9 LENGTH: 27 TENGTH:	Query Match Best Local S Matches 271 Qy 1 Db 61 Qy 121 Qy 121 Qy 181 Qy 241 Db 241 Db 241 Db 241 Db 241 NS-08-369-796-; 5 Sequence 12,

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APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
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Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                 NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKST NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFPX: 201 343-1684
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-852-091-12
                                                                                                                                                                             New Jersey
: USA
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                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                STATE:
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         GENERAL INFORMATION:

APPLICANT: James E. Darnell, Jr.

APPLICANT: Zhong Zhong Zhong

TITLE OF INVENTION: PUNCTIONALLY ACTIVE REGIONS OF SIGNAL

TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOOKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
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                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESQ., DAVId A.
REGISTRATION NUMBER: 26,742
REPRENCE/POCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                      STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 770 amino acids amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 271; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-369-796-12
                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                              COUNTRY:
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; Sequence 12, Application US/08820754
; Patent No. 5976835
GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
APPLICANT: Parioller, Christian W., APPLICANT: Fu, Xian-Yuan RESULT 4

Sequence 12, Application US/08852091 Patent No. 5883228 GENERAL INFORMATION: APPLICANT: James E. Darnell, Jr. APPLICANT: 21long Wen

RESULT 3 US-08-852-091-12

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347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Jersey
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APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jacker-
STREET: 411 u----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1388; DB 2; Length 770; 100.0%; Pred. No. 1.7e-118; tive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 19-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 19-MAR-1992
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 24-SEP-1993
ATTOMEX/AGENT INFORMATION:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTOMEX/AGENT INFORMATION:
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                              ADDRESSEE: Klauber & Jackson STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Jersey COUNTRY: USA ZIP: 07601 COMPUTER READABLE FORM: MEDIUM TYPER: RIOPPY disk COMPUTER: 1BM PC COMPATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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amino acid
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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107 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE 166
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0
                         APPLICANT: Darnell Jr., James E.

APPLICANT: Schindler, Christian W.

APPLICANT: Fu, Xian-Yuan

APPLICANT: Fu, Xian-Yuan

APPLICANT: Zhong, Zhong

TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN

TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber F. T.

STREEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1388; DB 3; Length 770; 100.0%; Pred. No. 1.7e-118; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185.
FILING DATE: 11-WAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR-1993
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 24-68P-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
US-08-956-652-12
; Sequence 12, Application US/08956652
; Patent No. 6013475
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Best Local Similarity 100.0
Matches 271; Conservative
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61 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
                                                                                                                                                                           121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
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0; Gaps
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APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Fu, Xian-Yuan
APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Schind Xian-Yuan
APPLICANT: All Hackensack Avenue
STREET: 411 Hackensack Avenue
Indels
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CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 12-NOV-1992
PRIOR APPLICATION NUMBER: US 07/864,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: WO US91/026,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson ESG., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
RELEPAX: 201 343-1684
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  0; Mismatches
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271; Conservative
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ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: New Jersey
COUNTRY: USA
  Matches
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                                                                                                                            LOOKVSYKGDPIVOHRPMLEERIVELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFT
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APPLICANT: Darnell Jr., James E.
APPLICANT: Fu, Xián-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Jong
APPLICANT: Men, Zilong
APPLICANT: Anney
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,869
                                                                                                                                                                                                                                                            347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORWATION:
NAME: JGCKGON EGG, DAVIG RESISTANTION NUMBER: 26,742
RESISTANTION NUMBER: 20,742
RESISTANTION NUMBER: 20,742
RESISTANTION NUMBER: 20,742
TELEPHONE: 201 487-5800
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LIRET: Klauber & Jackson
LIRET: 411 Hackensack Avenue
CITY: Hackensack Avenue
STATE: New Jersey
COUNTRY: USA
ZIP: 0760'
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/212,185
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Patent No. 6030808
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
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amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Darnel
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Patent No. 6235873

GENERAL INFORMATION:
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-25

CURRENT APPLICATION NUMBER: US/09/364,970

CURRENT PILING DATE: 1999-07-31

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 3

LEMCTH: 770
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Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                            100.0%; Score 1388; DB 3; Length 770; 100.0%; Pred. No. 1.7e-118; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
                                              LENGTH: 770 amino acids

17PE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-948-547-12
                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 271; Conservative
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-3
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Sequence '5, Application US/09364970

| Sequence '5, Application US/09364970
| Patent No. 6235873
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
| TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
| TITLE OF INVENTION: DYSPRCLIFFRATIVE CELLULAR CHANGES
| TITLE OF INVENTION: DYSPRCLIFFRATIVE CELLULAR CHANGES
| TITLE OF INVENTION: DYSPRCLIFFRATIVE CELLULAR CHANGES
| TITLE OF INVENTION: DATE: 1999-07-31
| CURRENT FILING DATE: 1999-07-31
| NUMBER OF SEQ ID NOS: 10
| SEQ ID NO 5
| LENGTH: 770
| LENGTH: 770
| TYPE: PRT
| ORGANISM: Mus musculus
| US-09-364-970-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
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APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; DB 3;
1.7e-118;
347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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; Pred. No. 1.7e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
100.0%;
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.0
Matches 271; Conservative
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CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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US-08-956-653A-12
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167 NIGDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
       SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
BRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
BRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAVE: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECHONE: 201 487-5800
TELEFPAX: 201 343-1684
                                                                                                      E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 770 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                         CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
       TITLE OF INVENTION:
                                                                                                      ADDRESSEE:
STREET: 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
PCT-US95-17025-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-212-185-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08212185

Patent No. 6605442

GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
ITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                 OFFWALLY SYSTEM: PC_DOS/MS-DOS SOFFWALE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/956,653A FILING DATE: TLING DATE: FILING DATE: CLASSIFICATION NUMBER: US 08/212,185 FILING DATE: 13-NOV-1994 APPLICATION NUMBER: US 07/980,498 FILING DATE: 23-NOV-1992 PRIOR APPLICATION NUMBER: US 07/854,296 FILING DATE: 19-MAR-1992 PRIOR APPLICATION NUMBER: US 07/854,296 FILING DATE: 19-MAR-1993 PRIOR APPLICATION NUMBER: US 08/126,588 FILING DATE: 19-MAR-1993 PRIOR APPLICATION NUMBER: US 08/126,588 FILING DATE: 24-SEP-1993 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: US 08/126,588 FILING DATE: 24-SEP-1993 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: US 08/126,588 FILING DATE: 24-SEP-1993 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: US 08/126,588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 1388; DB 3; Best Local Similarity 100.0%; Pred. No. 1.7e-118; Matches 271; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-195
TELECOMMUNICATION:
TELEPHONE: 201 487-5800
                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LELEFAX: 201 343-1684

TELEX: 133521
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 770 amin.
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-956-653A-12
                                      OPERATING SYSTEM:
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US-08-212-185-12
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Length 770;

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181 LQQKVSYKGDPIVQHRPMLEBRIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 AMEYVQKTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
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Pred. No. 1.7e-117;
1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B FILING DATE: 04-APR-1995 CLASSIFICATION NUMBER: US/08/416,581B FILING DATE: 04-APR-1995 FILING DATE: 04-APR-1994 FILING DATE: 04-APR-1994 ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
                                                                                                                                                     ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W.
Patent No. 5719042
GENERAL INFORMATION:
APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Akira, Shizuo
TITLE OF INVENTION: TRANSCRIPTION FACTOR APRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 0-37891
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moarefi, Ismail
Darnell, Jr., James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8, Application US/09012710; Patent No. 6087478; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,981
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APPLICANT: Moarefi, Ismail
APPLICANT: Darnell, Jr., Je
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.3
Matches 269; Conservative
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MOLECULE TYPE: protein
                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, 1
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                               CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                  ZIP: 20037
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                                APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Curt M. Horvath
APPLICANT: Curt M. Horvath
APPLICANT: Chong Zhong
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEGUNCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CARRENT APPLICATION DATA:
PTLING DATE: 28-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
RAGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELECHONE: 201 487-5800
TELECHAX: 201 343-1684
  , Application PC/TUS9517025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-08-416-581B-9
; Sequence 9, Application US/08416581B
                                                                                                                                                                                                                      ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 133521
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION;
                                                                                                                                                                                                                                                                                                                                       ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-17025-12
                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227
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IITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
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APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                        ZIP: 07601

MEDIUM TYPE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/09/012,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1377; DB 3;
Pred. No. 1.7e-117;
1; Mismatches 1;
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                                                                                                    ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201-487-5800
201-487-5800
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 770 amino acids STRE: amino acids STRANDEDNESS: sir...
TOPOLOGY: ''.
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Best Local Similarity 99.3
Matches 269; Conservative
                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
                                                                                                                                                                     New Jersey
: USA
                                                                                                                                    CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-012-710-8
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287 LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPM+PDRPLVIKTGVQFT 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 NLÓDDFDFNYKTLKSQGDMQDINGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/556,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

99.2%; Score 1377; DB 3;
Best Local Similarity 99.3%; Pred. No. 1.7e-117;
Matches 269; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
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                                                                            411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5, 2005, 14:58:52
                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/012,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 133521
INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                               CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Job time : 41.8094 secs
                                                                                                                                                COUNTRY: US/
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-556-273-8
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226

APPLICANT: Vinkemeier, Uwe
APPLICANT: Moarefi, Ismail
APPLICANT: Moarefi, Ismail
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A

Sequence 8, Application US/09556273 Patent No. 6312887 GENERAL INFORMATION:

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

5, 2005, 14:55:35 ; Search time 84.1694 Seconds (without alignments) 1245.251 Million cell updates/sec Мау Run on:

Title: Perfect score:

US-10-090-185-9 1388 1 RCLWEESRLLQTAATAAQQG.......INYQLKIKVCIDKDSGDVAA 271 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* 1: genesecn1000... •• Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aay72841 Mouse Sta	Aar72082 Mouse Sta	Aaw03176 Mouse STA	Aae22055 Human Sta	Abb57164 Mouse isc	Aae22054 Human Sta	Aae22056 Human pro	Aar82995 Mouse liv	Aay03768 Human STA	Aab12377 N-termina	Aae14652 Murine ST	Abg69497 Human bai		Adn04365 Antipsori	Adp54789 Human PRO	Aab58442 Lung canc	Add44738 Rat Prote	Aar82993 Human pla	Aab19964 Human sig	Aae15174 Human Sta	Add44740 Human Pro	Aay72846 Mouse Sta	Aay72847 Mouse Sta	Aay72850 Mouse Sta	Aay72863 Mouse Sta
QI	AAY72841	AAR72082	AAW03176	AAE22055	ABB57164	AAE22054	AAE22056	AAR82995	AAY03768	AAB12377	AAE14652	ABG69497	ABU10476	ADN04365	ADP54789	AAB58442	ADD44738	AAR82993	AAB19964	AAE15174	ADD44740	AAY72846	AAY72847	AAY72850	AAY72863
BB	4	~	~	Ŋ	Ŋ	Ŋ	ហ	~	7	m	S	ហ	9	ω	æ	٣	7	~	4	Ŋ	7	4	4	4	4
% Query Match Length	271	770	770	720	. 769	169	169	770	770	770	770	770	770	770	770	793	770	770	770	770	770	252	236	229	229
& Query Match	100.0	100.0	100.0	99.2	99.2	99.2	99.2	99.5	99.2	99.2	99.5	99.2	99.2	99.2	99.2	99.5	0.66	98.8	98.8	98.8	98.8	92.9	87.3	84.4	84.1
Score	1388	1388	1388	1377	1377	1377	1377	1377	1377	1377	1377	1377	1377	1377	1377	1377	1374	1372	1372	1372	1372	1290	1212	7	1168
Result No.	-	7	٣	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aay72862 Mouse Sta	Aay72861 Mouse Sta	Aay72860 Mouse Sta	Aay72854 Mouse Sta	Aay72851 Mouse Sta	Aay72855 Mouse Sta	Aay72848 Mouse Sta	Aay72849 Mouse Sta	Aay72856 Mouse Sta	Aag78526 Rat STAT-	Aay72852 Mouse Sta	Mouse	Abr59713 Human sig	Aar72079 Human Sta	Aaw03170 Human STA	Aaw62995 Human Sta	Abu04747 Human exp	Abu04735 Human exp	Abu04745 Human exp	Abu04743 Human exp
AAY72862	AAY72861	AAY72860	AAY72854	AAY72851	AAY72855	AAY72848	AAY72849	AAY72856	AAG78526	AAY72852	AAY72844	ABR59713	AAR72079	AAW03170	AAW62995	ABU04747	ABU04735	ABU04745	ABU04743
4	4	4	4	4	4	4	4	4	ß	4	4	9	N	N	0	9	9	ø	9
229	228	229	223	213	185	176	143	129	749	128	268	680	712	712	712	712	712	712	712
84.1	83.4	82.6	82.3	78.8	67.9	64.8	52.1	48.2	47.1	47.0	46.6	46.6	46.6	46.6	46.6	46.6	46.6	46.6	46.6
1167	1157.5	1146	1142	1094	943	899	723	699	654	653	647	647	647	647	647	647	647	647	647
26	27	28	53	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

```
Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                   Mouse Stat3 protein fragment #2 (107-377 amino acids).
    AAY72841 standard; protein; 271 AA.
                         (first entry)
                                                                   Mus musculus.
                         31-MAY-2001
               AAY72841;
                                                          therapy.
AAY7284
```

Location/Qualifiers Key Region

24. .48 /note= "Stat3-c-Jun interaction region 1; corresponds 130-154 position of Stat3 protein" 236. .252 Region

to

/note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"

WO200116605-A2.

08-MAR-2001

30-AUG-2000; 2000WO-US023822.

99US-00387418 31-AUG-1999;

(UYRQ) UNIV ROCKEFELLER.

Darnell JE; Wrzeszcynska MH, Horvath C, Zhang X,

WPI; 2001-226705/23.

Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.

Claim 65; Page 67-68; 86pp; English.

The present sequence is mouse Stat3 protein fragment containing 107-377 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the call extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a

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                                                                                                                                                                                                                                                              NIQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
                                                                                                                                                                                                                                                                                                                                  180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal transducer and activator of transcription, STAT, 19sf6, Stat3, receptor recognition factor, transcription factor, cellular debilitation, derangement, dysfunction, interferon-gamma.
transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysprolifrative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, colled-coil domain, bind binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.
                                                                                                                                                                                                                                                                                                      AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE
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                                                                                                                                Length 271;
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                                                                                                                                100.0%; Score 1388; DB 4; 100.0%; Pred. No. 2.7e-116;
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                                                                                                                                                                                                                                                                                                                                                                                                                    TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
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                                                                                                                                                            0; Mismatches
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94US-00212184.
94US-00212185.
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(first entry)
                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Stat3 (19sf6).
                                                                                                                               Query Match
Best Local Similarity
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                                                                                                    Sequence 271 AA;
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27-SEP-1995
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                       A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080) (Stat1) that was responsive to interferon-gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AAQ89339-40) were cloned in plasmids 13sf1 and 19sf6 and encoded proteins termed Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-2003 to correct PN field.)
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disease; antagonist; therapy.
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                                                                                                                                                                                              Length 770;
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                                                                                                                                                                                            100.0%; Score 1388; DB 2;
100.0%; Pred. No. 1.1e-115;
ive 0; Mismatches 0;
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/label= DNA binding_domain
/note= "Claim 3, page 110"
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Claim 1; Page 107-110; 160pp; English.
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                                                                                                                                                                                                            Best Local Similarity 100.
Matches 271; Conservative
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                                                                                                                                                                     Sequence 770 AA;
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                                                                                                                                                                                                 Query Match
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Domain
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                                                                                                           STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from ligand-activated receptor kinase complexes followed by nuclear translocation and DNA binding to activate transcription. Recombinant STAT4 can be obtd. using cDNA clone 198f6 (AAT31278) obtd. from splenic/thymic cells. STAT4 includes a DNA-binding domain (see also AAW03167) capable of both receptor recognition and message delivery via DNA binding in a receptor-ligand specific manner. STAT proteins and their DNA binding domains (see also AAW03165-75) are useful for screening antagonists used to inhibit STAT-mediated signal transduction and
                                                                                                                                                                                                                                                                                                                                                 LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
                                                                                                                                                                                                                                                                                                                                                                                      NLQDDFDFDYYYTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
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                       New STAT protein DNA-binding domain peptide(s) - useful for diagnosing, preventing or treating cellular dysfunction, e.g. oncogenesis, inflammation, parasitic disease or autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis, vascular occlusion; hypotais stroke; angiogenesis, myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; drave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion; Statbeta.
                                                                                                   Mouse signal transducer and activator of transcription (STAT) protein
                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                  Length 770;
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                                                                                                                                                                                                                                                                                 100.0%; Score 1388; DB 2; 100.0%; Pred. No. 1.1e-115;
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                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                          Disclosure; Page 87-90; 138pp; English
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                                                                                                                                                                                                                               activation of transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                         Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Stat3beta protein.
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                       Sequence 770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing, bypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, tissue ischaemia in the lower extremities, infarction, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chirogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy mitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus erythematosus, multiple scleroderma, polymyositis, chronic active hepatitis, sixed connective tissue disease, primary biliary cirrhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic addison's disease, vitiligo, gluten-sensitive enteropathy, autoimmune neutropenia, myaathenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, vietulador grathritis, cirrhosis, pemphigus wilders edposit disease. The method is useful in preventing or treating chere deposit disease. The method is useful in preventing or treating appecification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMEYVOKTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE
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Pred. No. 9.6e-115;
1; Mismatches 1;
713. .714
/note= "Encoded by ACA CCA TTC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dalton W;
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   Misc-difference 713
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(UYSF-) UNIV SOUTH
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hes 269;
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120 226

167 NLQDDFDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 226

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conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57347) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
                   LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
LQQKVSYKGDP1VQHRPMLEER1VELFRNLMKSAFVVERQPCMPMHPDRPLV1KTGVQFT
                                                                                                                                                                                                                                                                                                                      Mouse ischaemic condition related protein sequence SEQ ID NO:398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for examining ischaemic
                                                                                                                                                                                                                                                                                                                                                       Mouse, ischaemia, compressive ischaemia, occlusive ischaemia, vasospastic ischaemia, ischaemic condition; ischaemic disease.
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                                                                                             TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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                                                                          TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA
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                                                                                                                                                                                                        ABB57164 standard; protein; 769 AA
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                                                                                                                                                                                                                                                                                 (first entry)
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1 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE

Matches 269; Conservative

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Similarity

Local

Gaps

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61 NLQDDFDFNYXTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120

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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, trauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, subcotionion, control obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
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  180
                                       286
                                                                               240
                                                                                                    287 LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
                    227 AMEYVQKTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE
  121 AMEYVOKTLIDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLOTROQIKKLEE
                                                                               LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVBRQPCMPMHPDRPLVIKTGVQFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia, stroke; anglogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carrinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.
                                                                                                                                                              TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
                                                                                                                                                                                   347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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                                                                                                                                                                                                                                                                                                        AAE22054 standard; protein;
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nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus erythematosus, multiple sclerosis, insulin dependent diabetes mellitus, Siogran's syndrome, scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, pennicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, ilpoparacoma, degenerative diseaters, physoproliferative disorders, physologiaera, physologiaera,
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Sequence 769 AA;

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107 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE 166
                                                                                                                                          NLODDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
                                                                                                                                                                AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
                                                                                                                                                                                                                                   AMEYVQKTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 286
                                                                                                                                                                                                                                                                                   LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
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                                                                       RCLWEESRILLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
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99.2%; Score 1377; DB 5; Length 769; 99.3%; Pred. No. 1e-114; ive 1; Mismatches 1; Indels (
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                                  Conservative
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les 269; Conserv
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AAE22056 standard; protein; 769 AA (first entry) 25-JUL-2002 AAE22056;

Human protein related to angiogenesis regulation.

immune response; Stat1; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; anglogenesis; myocardial infarction; hypoglycaemia; inflammation, chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; theumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disease; gene therapy; growth deficiency; cirrhosis; hypoproliferative diseacer; lesion. Human; signal transducer and activator of transcription 3; ischaemia;

120

226

166

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286

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346

TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271

241

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Homo sapiens

WO200220032-A1

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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stati). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, tissue ischaemia in the lower extremities, infarction, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, coclusion, prental or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, nitrogen necrosis, proliferative andiologathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating symptome, antoimmune disease such as systemic lupus crythematosus, multiple sclerosis, insulin dependent diabetes mellitus, sjogren's syndrome, sclerosis, insulin dependent diabetes mellitus, sjogren's syndrome, sclerosis, insulin dependent diabetes mellitus, connective tissue disease, primary bilary cirrhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, discoid lupus, ulcerative colitis and ciscase, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune thyroiditis, idiopathic Addison's disease, recommens e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, connective disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human controller angiogenesis regulation
                                                                                                                                                                                                                                                                    Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
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1; Mismatches
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                                                                            08-SEP-2000; 2000US-0231212P
                                         10-SEP-2001; 2001WO-US028254
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(UYSF-) UNIV SOUTH FLORIDA.
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                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a mouse acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (IL-6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA library using a polymerase chain reaction product (amplified using primers derived from an IL-6-treated mouse liver peptide) as a probe. ARPF-inhibitors, e.g. antibodies, antisense oligonucleotides or ribozymes, may be used to treat diseases induced by IL-6, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                 New acute phase response factor - for developing inhibitory agents for treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
                                                                                                                  Mouse; acute phase response factor; transcription factor; interleukin-6; signal transmission; liver; antibody; antisense; ribozyme; antiinflammatory; antitumor; hypotensive; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RCLWEESRLIQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1377; DB 2;
Pred. No. 1e-114;
1; Mismatches 1;
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TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                  Mouse liver acute phase response factor.
                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 20-22; 31pp; English.
                                            AAR82995 standard; protein; 770 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.2%;
                                                                                                                                                                                                                95EP-00104670.
                                                                                                                                                                                                                                 94JP-00065825.
                                                                                (first entry)
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Matches 269; Conservative
                                                                                                                                                                                                                                                                      Akira S, Kishimoto T;
                                                                                                                                                                                                                                                   (KISH/) KISHIMOTO T.
                                                                                                                                                                                                                                                                                       WPI; 1995-346089/45.
N-PSDB; AAT05619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypertension, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 770 AA;
                                                                                                                                                                                                                                  04-APR-1994;
                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                29-MAR-1995;
                                                                                 25-MAR-1996
                                                                                                                                                                           EP676469-A2
                                                                                                                                                                                             11-0CT-1995
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Best Local &
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                                                               AAR82995;
                                                                                                                                                                                                                                                                                                                                    diseases
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The present sequence represents a predominant allelic variant of human Signal Transducer and Activator of Transcription 3 (STAT3) protein, an intracellular transcription factor which mediates IL-6 signals. The encoding sequence differs from the original published human STAT3 gene sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3 DTA molecule can be used for the recombinant expression of the variant. STAT3 protein is useful as a medicament or pharmaceutical composition for treatment of autoimmune or inflammatory diseases
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                                                                                                                                                                                                                                                                                                                                                                                             Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6; intracellular transcription factor; interleukin-6; medicament; variant; pharmaceutical; autoimmune disease; inflammatory; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
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347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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                                                                                                                                                                            AAY03768 standard; protein;
                                                                                                                                                                                                                                                                                                                                                Human STAT3 allelic variant
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Best Local Similarity 99.3
Matches 269; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-192664/17.
N-PSDB; AAX29281.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater than S. O Angstrome. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3 dimensional structure determined for the crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New crystals of an N-terminal fragment of a signal transducer and activator of transcription that effectively diffracts x-rays, useful for drug screening and development.
                                                                                                                                                          {\tt STAT}_i signal transducer and activator of transcription, crystal, drug design, murine.
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                                                                                                                                                                                                                                                                                               alpha helix
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N-terminal domain of murine STAT-3 protein.
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                                                                                                                                                                                                                                                                                                3(10) helix of
                                                                                                                                                                                                                                                              .2. .21
/label= Alpha helix 2
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/label= Alpha helix 3
                                                                                                                                                                                                                                                                                                                                                                                                     77. .96
/label= Alpha helix 7
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/label= Alpha helix 1
                                                                                                                                                                                                                                                                                                                                            helix 4
                                                                                                                                                                                                                                                                                                                                                        43. .47
/label= Alpha helix 5
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/label= Alpha helix 8
                                                                                                                                                                                                                                                                                                                                                                                            helix
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                                                                       AAB12377 standard; peptide; 770
                                                                                                                                                                                                                                                                                                                                35. .40
/label= Alpha
                                                                                                                                                                                                                                                                                                                                                                                 50. .73
/label= Alpha
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                                                                                                                    (first entry)
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/label=
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                                                                                                                    08-NOV-2000
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              347
                                                                                            AAB12377;
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99.2%; Score 1377; DB 3; Length 770;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to methods for detecting compounds that bind to signal transducer and activator of transcription (STAT) proteins for the discovery and development of new drug compounds based on the structural properties of the protein crystal. The methods include: identifying a compound that enhances or diminishes the binding of the dimeric STAT proteins to each other and/or their nucleic acid binding site; or identifying a compound that enhances or diminishes the binding of the dimeric STAT proteins to each other and/or their nucleic acid binding site; or identifying a compound that enhances or diminishes the ability of STAT protein dimers to induce the expression of a gene operably under
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    .130
/note= "Conserved N-terminal domain of the STAT family"

                                                                                                                                                                                               227 AMEYVQXTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE
                                                                                                                                                                                                                                                            107 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
                                                                                                                NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
                                                                                                                                NLODDFDFNYKTLKSOGDMODLNGNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGILIS
                                                                                                                                                                              AMEYVOKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE
                                                                                                                                                                                                                                           181 LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying compounds that bind to signal transducer and activator of transcription proteins, useful for the production of new drugs.
                     Gaps
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   Pred. No. 1e-114;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                          TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 viral disease; growth retardation; murine
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAE14652 standard; protein; 770
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Best Local Similarity
Matches 269; Conserv
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the control of a promoter containing at least two adjacent weak binding sites for STAT protein dimers. The methods are used for identifying new daugs. An antagonist of STAT N-terminal dimeric interactions that inhibits the binding of the STAT dimers to adjacent weak binding sites on a promoter of a gene, could be useful as drugs in the treatment of diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other hand, an agonist of N-terminal dimeric interactions between STAT dimers, can be used as drugs in the treatment of diseases e.g. anaemia, neutropaemia, thrombocytopaemia, cancer, obesity, viral diseases and growth retardation. The present sequence is murine STAT3 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, yeast two-hybrid assay, adipocyte, bait protein; NIDDM,
non-insulin diabetes mellitus, obesity, selected interacting domain, SID,
protein-protein interaction map, PIM, anorectic, metabolic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLODDFDFNYKTLKSGGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
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Best Local Similarity 99.3%;
Matches 269; Conservative
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(CNRS ) CENT NAT RECH SCI.
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The invention relates to a complex or procein-procean interactions appropriate to a complex or procein-procean interaction map, PIM) in adipocyte cells as defined in the specification, or polynucleotides in adipocytes encoding for the polypeptides. Also included are a recombinant cell expressing the interacting polypeptides and a method of selecting a modulating compound in adipocyte cells, by cultivating a recombinant host cell on a selective medium containing a modulating compound and a reporter gene the expression of which is toxic for the recombinant host cell which is transformed with two vectors, where the first vector comprises a polynucleotide encoding a first hybrid polypeptide and DNA binding domain comprise comprising a polynucleotide encoding a second chyprid polypeptide and an activating domain that activates the toxic reporter gene, when the first and second hybrid polypeptides interact and selecting the modulating compound which inhibits the growth of the recombinant host cell (i.e. using the yeast two-hybrid system). The complexes are useful for identifying compounds that modulate the protein-complexes are useful for treating obesity and metabolic diseases. The interactions between the proteins obesity or metabolic diseases. The interactions between the proteins obesity or metabolic diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLODDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the complex further define a set of selected interacting domains, SID. The present sequence represents a member of the protein complex of the invention, used as the bait protein in the yeast two-hybrid assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 NLODDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
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drug screening; STAT-STAT dimer interaction; STAT3.
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                                                                 protein-protein
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                                                                 relates to a complex of
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/label= alpha_helix_1
12. .21
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                      Claim 1; Page 54; 125pp; English.
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les 269; Conservative
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The invention relates to a crystal of an N-terminal domain of signal transducer and activator of transcription (STAT) protein, where the crystal effectivaly diffracts X-rays for the determination of the atomic coordinates of the N-terminal domain of the STAT protein to a resolution of greater than 5.0 Angstrom. The methods and compositions are useful for the design and screening of drugs that enhance or inhibit STAT-STAT dimer interactions. The present sequence represents the amino acid sequence of mouse STAT3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVU 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLODDFDFNYKTLKSOGDMODLNGNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New crystal having an N-terminal domain of a STAT protein performing X-ray crystallographic studies, useful for screening drugs that enhance or inhibit STAT-STAT dimer interactions.
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Pred. No. 1e-114;
1; Mismatches 1; Indels
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              note= "Residues 19-21 form a 3 helix"
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                                                                                                                         68
                                                                                                                                                                        90
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                                                                                                                                                                            packing of the coiled-coil"
                                                                                                                                                                                                                                                                                                                                                                                                            Darnell JE,
                                                                      13. .47
| label= alpha_helix_5
                                                                                                          /label= alpha_helix_6
/note= "Residues 57, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 25-26; 46pp; English.
                                               35. .40 _ _ _ /
/label= alpha_helix_4
                                   alpha_helix_3
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 'label= alpha_helix_
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24-APR-2000; 2000US-00556273.
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DARNELL J E.
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Matches 269; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                   Wood .WI;
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                                                                                                                                                                                                                                                                                                                                  Jackman J, Schoenfeld J, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 770;
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TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
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                                                                                                                                                Antipsoriatic protein sequence #377.
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                                                                              ADN04365 standard; protein; 770
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Best Local Similarity
Matches 269; Conserv
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                                                                                                                                                                                             Homo sapiens.
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Sequence 770 AA;

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human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritic; antiathematic; antidabetic; antiinflammatory; antipsoriatic; antithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
                                                             Human PRO protein sequence SEQ ID NO:765.
               ADP54789 standard; protein; 770 AA
                                                                                                                                                                                        28-OCT-2003; 2003WO-US034381.
                                                                                                                                                                                                      29-OCT-2002; 2002US-0422472P
                                             (first entry)
                                                                                                                           virucide; gene therapy
                                                                                                                                                                                                                                     3, Clark H,
Wu TD;
                                                                                                                                                                                                                                                            WPI; 2004-376182/35.
N-PSDB; ADP54788.
                                                                                                                                                         WO2004039956-A2
                                                                                                                                          Homo sapiens
                                             18-NOV-2004
                                                                                                                                                                        13-MAY-2004.
                                                                                                                                                                                                                                      Aggarwal S,
                               ADP54789;
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RESULT 15
ADP54789
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(GETH) GENENTECH INC

Gurney AL, Schoenfeld J, Williams PM;

New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response.

Claim 1; SEQ ID NO 765; 3009pp; English.

The present invention describes an isolated PRO nucleic acid (I). Also described: (1) a vector comprising (I); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the colypeptide of (4) fused to a heterologous amino acid sequence; (6) an antibody which specifically binds to a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4), an agonist or antagonist of the polypeptide or an antibody that binds to the composition of matter of the polypeptide or an antibody that binds to the polypeptide or an antibody that binds to the composition of matter of (7); (9) a method of treating an immune related disease in a mannal; (10) a method for determining the presence of a PRO polypeptide in a sample suspected of having the polypeptide; (11) a method of distanting the presence of a PRO polypeptide in as ample suspected of simulating the inflammatory immune response in mammal; (12) a method of identifying a compound that inhibits or minces the activity of or expression of a gene encoding a PRO polypeptide in mammal. The procession of the immune response in a mammal. The procession of the immune response in a mammal of the inflammatory immune in the procession of the immune response in a mammal. The procession of the immune response in a mammal of the inflammatory immune in the procession of the immune response in a mammal. The procession of the immune response in a mammal of the inflammatory immune in the procession of the immune response in a mammal. The procession of the immune response in a mammal of the inflammatory immune in the procession of the immune response in a mammal. The procession of the immune response in a mammal of the inflammatory immune in the procession of the immune response in a mammal. The procession of the immune response in a mammal of the inflammatory immune in the procession of the immune response in a method of inflammatory immune in the procession of the immune PRO Sequences have antiallergic, antianamic, antiarthritic, antiasthmatic, antialergic, antianamic, antiarthritic, antialergic, antiinflammatory, antipsoriatic, antithyroid, CNS, dermatological, gastrointestinal, haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular, nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and virucide activities, and can be used in gene therapy. The nucleic acid (I) and the encoded polypeptides, compositions, kits and methods are useful in diagnosing and treating an immune response. The present sequence represents a human PRO protein from the present invention.

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181 LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
                                                                                                                                                                                                                                                                                                                               107 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE 166
                                                                                                                                                      NLODDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
                                                                                                                                                                                      167 NLÓDDFDFNYKTLKSGGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 226
                                                                                                                                                                                                                                AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
                                                                                                                                                                                                                                                                   227 AMEYVOKTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 286
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                                                                            1 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
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99.2%; Score 1377; DB 8; Length 770; ilarity 99.3%; Pred. No. 1e-114; Conservative 1; Mismatches 1; Indels
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Best Local Similarity
Matches 269; Conserv
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Mouse STA Rat Prote Human Pro Human bai Human Sta Mouse STA

Antipsori Human PRO

Aae14652 Aae15174 Abu10476 Abu10476 Add44738 Add44740 Adb64789 Aab54789 Aab54789 Aab54789 Aab54789 Aab64789 Aab64789 Aab64789 Aab64789 Aaw01102

Lung canc Mouse Sta Breast ca Signal tr Signal tr

Human sig Human Sta Breast ca Human PRO

Protein e Human NF-Human NF-

Aab19965 1 Aae15175 1 Abr47599 1 Ad182891 1 Adp13003 1 Adr14069 1 Adr14361 1

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ABG69497
AAR15174
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ADF572855
ABR472855
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AAR1102
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                             May 25, 2005, 17:14:45; Search time 50.566 Seconds (without alignments) 726.619 Million cell updates/sec
                                                       1 VQDLEQKMKVVENLQDDFDF.......vvQKTLTDEELADWKRRPEI
    GenCore version 5.1.6
Copyright (c) 1993 - 2005. Compugen Ltd.
                      OM protein - protein search, using sw model
                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                               US-10-090-185-21
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ALIGNMENTS

Total number of hits satisfying chosen parameters:

length: 0 length: 200000000

Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04: geneseqp1980s:* geneseqp1990s:*

Database

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:*

2105692 seqs, 386760381 residues

Title: Perfect score:

Run on:

Seguence:

Scoring table:

Searched:

Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis; Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein. Mouse Stat3 protein fragment #11 (155-249 amino acids). Darnell JE; Zhang X, Horvath C, Wrzeszcynska MH, AAY72853 standard; protein; 95 AA Claim 65; Page 78; 86pp; English. 31-AUG-1999; 99US-00387418. 30-AUG-2000; 2000WO-US023822 (first entry) (UYRQ) UNIV ROCKEFELLER WPI; 2001-226705/23. WO200116605-A2 Mus musculus. 31-MAY-2001 08-MAR-2001. AAY72853; therapy.

Mouse Human Aay72852 Aay72849 Aay72849 Aay72849 Aay72861 Aay72861 Aay72862 Aay72862 Aay72863 Aay72864 Aay72847 Aay72841 Aay72842 Aae22054 Aay20954 Aay2082 Aae22054 Aay20954 Aay2

The present sequence is mouse Stat3 protein fragment containing 155-249 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, colled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain

Sequence 95 AA;

N-termina Human sig

Mouse Human Mouse

AAE22055 ABB57164 AAE22054

AAR82995 AAR82993 AAY03768 AAB12377

AAB19964

AAE22056

us-10-090-185-21.rag

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AAY72849 standard; protein; 143 AA.
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                                            1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                      1 VQDLEQKWKVVENLQDDFDFDYKTLKSQGDWQDLNGNNQSVTRQKWQQLEQMLTALDQMR
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Score 477; DB 4; Length 95; Pred. No. 5.9e-41;
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                      Indels
                                                                                                                                                                                                                                  Mouse Stat3 protein fragment #10 (155-282 amino acids)
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100.0%; Pred. No. 8.3e-41;
ive 0; Mismatches 0;
                                                                                                   RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
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100.0%; Score 477;
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           100.0%;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is mouse Stat3 protein fragment containing 107-249 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                                                                                                                                                                           /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"
                                             Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
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Mouse Stat3 protein fragment #7 (107-249 amino acids)
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100.0%; Pred. No. 9.5e-41;
ive 0; Mismatches 0;
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                                                                                                                                                                                                          Location/Qualifiers
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nes 95; Conservative
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1. .25
/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acids of Stat3 protein. This Stat3 fragment showed very weak binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, colled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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/note= "Stat3-c-Jun interaction region 2; corresponds to
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100.0%; Pred. No. 1.5e-40;
iive 0; Mismatches 0;
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                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                          Zhang X, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-226705/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 213 AA;
                                                                                                                                                                                  WO200116605-A2
                           Mus musculus.
                                                                                                                                                                                                                                                                                                                       31-AUG-1999;
                                                                                                                                                                                                                              08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY72854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                            Region
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                                                                       Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                          24...48
/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is mouse Stat3 protein fragment containing 107-282 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis; therapy.
                                                                                     Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                            Mouse Stat3 protein fragment #6 (107-282 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse Stat3 protein fragment #9 (130-342 amino acids).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Darnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wrzeszcynska MH,
                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 65; Page 74-75; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY72851 standard; protein; 213
                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-2000; 2000WO-US023822.
31-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-226705/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 176 AA;
                                                                                                                                                                                                                                                                                                                                       WO200116605-A2
                                                                                                                                                                                Mus musculus
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The present sequence is mouse Stat3 mutant protein fragment containing 130-358 amino acids of Stat3 protein. This mutant is obtained by replacing Thr 346 with Ala, Lys 348 with Ala and Arg 350 with Ala in the Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-un and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain,

    .25
/note= "Stat3-c-Jun interaction region 1; corresponds to

             /note= "Wild type Lys substituted with Ala; corresponds to 348 position of Stat-3 protein"
                                                                                                                   /note= "Wild type Arg substituted with Ala; corresponds to 350 position of Stat-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis; therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKNQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for use in modulating the interaction between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JE;
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100.0%; Pred. No. 1.6e-40;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying an agent for use in modulating the transcription factor c-Jun and a Stat3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 66; Page 84-85; 86pp; English.
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                                                                                                                                                                                                                                                                                                                                                    30-AUG-2000; 2000WO-US023822
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Query Local Similarity 100...
Best Local Similarity 100...
Then 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang X, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-226705/23.
                                                                                            Misc-difference 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 228 AA;
Misc-difference
                                                                                                                                                                                                                          WO200116605-A2
                                                                                                                                                                                                                                                                                                                                                                                                                   31-AUG-1999;
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                                                                                                                                                                                                                                                                                     08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY72860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY72860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is mouse Stat3 protein fragment containing 155-377 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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    .25
/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild type Thr substituted with Ala; corresponds to 346 position of Stat-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse, Stat3 protein, transcription factor, c-Jun, gene transcription, cellular transformation, dysproliferative disease, cancer, psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213. .229
/note= "Stat3-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                     Darnell JE;
   342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 477; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 65; Page 79; 86pp; English.
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                                                                                                                                                                                                                                                           99US-00387418
                                                                                                                                                                                            30-AUG-2000; 2000WO-US023822
                                                                                                                                                                                                                                                                                                                       (UYRQ ) UNIV ROCKEFELLER
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                                                                                                                                                                                                                                                                                                                                                                                     Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-226705/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 223 AA;
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                                                                  WO200116605-A2
                                                                                                                                                                                                                                                           11-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-2001
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Region

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1. .25
//note= "Stat1-c-Jun interaction region 1; corresponds to //note= "position of Stat3 protein"
213. .229
//note= "Stat1-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is mouse Stat3 protein fragment containing 130-358 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of transformation. These identifying agents are used in the treatment of Stat protein comprises the N-terminal domain, coiled-coil domain, bind binding domain, linker domain, SH2 domain and transactivation domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 85
                                                                                                         Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VQDLEQKWKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
                                                                  Mouse Stat3 protein fragment #8 (130-358 amino acids)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Darnell JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 477; DB 4; 100.0%; Pred. No. 1.6e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 65; Page 76-77; 86pp; English.
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY72863 standard, protein; 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-2000; 2000WO-US023822.
                        (first entry)
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Les 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang X, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-226705/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             WO200116605-A2
                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-AUG-1999;
                        31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130-358 amino acids of Stati protein. This mutant is obtained by replacing lead and Arg Statis protein. This mutant is obtained by replacing lea 148 with Ala, Val 151 with Ala, Thr 346 with Ala, Lys 348 with Ala and Arg 350 with Ala in the Statis protein. The invention relates to methods for identifying increacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-un and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the preatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comperies the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation
                                                                                                                                                                                                                                       t
                                                                                                                                                                                                                                                                                              /note= "Wild type Lys substituted with Ala corresponds to 348 position of Stat-3 protein"
                                                                                                                                                                                                                                                                                                                                                              /note= "Wild type Arg substituted with Ala corresponds to 350 position of Stat-3 protein"
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                                         /note= "Wild type Leu substituted with Ala; corresponds to 148 position of Stat-3 protein"
                                                                                                                                                                                             /note= "Wild type Thr substituted with Ala corresponds 346 position of Stat-3 protein"
                                                                                                       /note= "Wild type Val substituted with Ala corresponds 151 position of Stat-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence is mouse Stat3 mutant protein fragment containing
                                                                                                                                               213. .229
/note= "Stat3-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Darnell JE;
130-154 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wrzeszcynska MH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-2000; 2000WO-US023822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00387418
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Horvath C,
                                                                                                                                                                                                                                                                                                                                             Misc-difference 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-226705/23
                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 229 AA;
                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                            WO200116605-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY72850
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Length 229; Indels

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Key Region

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The present sequence is mouse Stat3 mutant (L148A) protein fragment containing 130-158 amino acids of Stat3 protein. This mutant is obtained by replacing Leu 148 with Ala in Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jum and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain

    .25
/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"

                                                                                                                                                                                                                                                                                                          to 148 position of Stat-3 protein"
213. .229
/note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                      /note= "Wild type Leu substituted with Ala; corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 VQDLEQKOMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                         Mouse, Stat3 protein, transcription factor, c-Jun, gene transcription, cellular transformation, dysproliferative disease, cancer, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 477; DB 4; 100.0%; Pred. No. 1.6e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 66; Page 85; 86pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-2000; 2000WO-US023822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00387418.
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                                                                                        therapy; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 229 AA;
                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                          WO200116605-A2
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                                                                                                                                    Mus musculus
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Best Local S
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                                                                                                                                                                                                                                                      /note= "Wild type Val substituted with Ala corresponds to
151 position of Stat-3 protein"
213. .229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is mouse Stat3 mutant (V151A) protein fragment containing 130-358 amino acids of Stat3 protein. This mutant is obtained by replacing Val 151 with Ala in Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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                                           Mouse, Stat3 protein, transcription factor; c-Jun; gene transcription, cellular transformation, dysproliferative disease; cancer; psoriasis; therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VODLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR

    .25
/note= "Stat3-c-Jun interaction region 1; corresponds
130-154 position of Stat3 protein"

                                                                                                                                                                                                                                                                                                                                                        /note= "Stat3-c-Jun interaction region 2; corresponds 342-358 position of Stat3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
    Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Darnell JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 477; DB 4;
pred. No. 1.6e-40;
imarches 0;
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                                                                                                                                                                               cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 66; Page 86; 86pp; English.
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nes 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-226705/23.
                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                          WO200116605-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-AUG-1999;
                                                                                                                                        Mus musculus
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Darnell JE;

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RESULT 11 AAY72862

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Length 229; Indels

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Key Region

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49 VQDLEQKAKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is mouse Stat3 protein fragment containing 107-358 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods transcription factor such as c-Jun and a Stat protein between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of the sproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                              236. .252
/note= "Stat3-c-Jun interaction region 2; corresponds to
342-358 position of Stat3 protein"
                                                                    /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 477; DB 4; Length 252; larity 100.0%; Pred. No. 1.8e-40; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Stat3 protein fragment #2 (107-377 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Darnell JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang X, Horvath C, Wrzeszcynska MH,
                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY72841 standard; protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 65; Page 73; 86pp; English
                                                                                                                                                                                                                                                                                                 30-AUG-2000; 2000WO-US023822.
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les 95; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is mouse Stat3 protein fragment containing 107-342 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                     24. .48
/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"
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                                          Mouse, Stat3 protein, transcription factor; c-Jun; gene transcription, cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
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Mouse Stat3 protein fragment #5 (107-342 amino acids).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wrzeszcynska MH,
                                                                                                                                                                                Location/Qualifiers
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1es 95; Conservative
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                                                                                                                                      Mus musculus.
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Query Match

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completed: May 25, 2005, 17:36:34
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                                                                                                                                                                                                                                                                                                                                              The present sequence is mouse Stat3 protein fragment containing 107-377 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a stranscription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal transducer and activator of transcription; STAT; 19sf6; Stat3; receptor recognition factor; transcription factor; cellular debilitation; derangement; dysfunction; interferon-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VODLEQKWKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 60
/note= "Stat3-c-Jun interaction region 1; corresponds 130-154 position of Stat3 protein" 236. .252 //note= "Stat3-c-Jun interaction region 2; corresponds 342-358 position of Stat3 protein"
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                                                                                                                                                                                                                          Wrzeszcynska MH, Darnell JE;
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                                                                                                                                                                                                                                                                                                                         Claim 65; Page 67-68; 86pp; English
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                                                                                                                                         30-AUG-2000; 2000WO-US023822
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                                                                                   WO200116605-A2
                                                                                                                                                                    31-AUG-1999;
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27-SEP-1995
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A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080) (Stat1) that was responsive to interferon-gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AAQ89339-40) were cloned in plasmids 13sfl and 19sff and encoded proteins termed Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VODLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 107-110; 160pp; English.
                                                                                                                                                                                                                                  Shuai K,
                                             93US-00126588.
93US-00126595.
94US-00212184.
94US-00212185.
94WO-US010849
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nes 95; Conservative
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                                                24-SEP-1993;
24-SEP-1993;
                                                                                                   11-MAR-1994;
                                                                                                                           11-MAR-1994;
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May 25, 2005, 17:25:01; Search time 11.8868 Seconds (without alignments) 596.600 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20,
Sequence 17,
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Sequence 19,
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1 VQDLEQKMKVVENLQDDFDF......YVQKTL/TDBELADWKRRPEI
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(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-387-418A-19
US-09-387-418A-29
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US-08-387-418A-14
US-08-387-418A-14
US-08-387-612
US-08-36-65-12
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US-08-36-86-12
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PCT-US95-17025-12
US-08-416-581B-1
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Maximum Match 100%
Listing first 45 summaries
                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wreseaczynska, Melissa H
APPLICANT: Hyrvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
FILE REFERENCE: 600-1-253
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
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US-08-416-581B-9
US-09-012-710-8
US-09-087-46-6
US-09-556-242-2
US-09-526-542-2
US-09-17-800A-6
US-09-17-800A-6
US-09-387-418A-23
US-08-387-418A-23
US-08-387-418A-23
US-08-387-418A-23
US-08-918-46-2
US-09-387-418A-23
US-09-387-418A-23
US-09-387-418A-23
US-09-387-418A-23
US-09-387-418A-23
US-09-387-418A-23
US-09-387-418A-23
US-09-972-800A-8
US-09-972-800A-8
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APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Waresezczynska, Melissa H
APPLICANT: Horveth, Curt M
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT APLICATION NUMBER: US/09/387,418A
WUMBER OF SEQ ID NOS: 43
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; Sequence 21, Application US/09387418A
; Patent No. 6391572
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US-09-387-418A-20
; Sequence 20, Application US/09387418A
; Patent No. 6391572
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; ORGANISM: Mus musculus
US-09-387-418A-21
                                                 SOFTWARE: PESEQ ID NO 21
LENGTH: 95
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Sequence 19, Application US/09387418A

Sequence 19, Application US/09387418A

Patent No. 6391572

GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wizeszzynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-223

CURRENT APPLICATION NUMBER: US/09/387,418A

CURRENT APPLICATION NUMBER: US/09/387,418A

CURRENT PILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, James E
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: 1999-08-31
CURRENT APPLICATION NUMBER: US/09/387,418A
SOURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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100.0%; Score 477; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 1e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0
                                                                                            Length 176;
                                                                                                                                               Indels
                                                                                            Query Match 100.0%; Score 477; DB 3; Best Local Similarity 100.0%; Pred. No. 8.2e-45; Matches 95; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                         109 RSIVSELAĞLLSAMEYVQKTLTDEELADWKRRPEI 143
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CRGANISM: Mus musculus
US-09-387-418A-19
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                          ORGANISM: Mus musculus
                                               US-09-387-418A-16
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LENGTH: 223
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TYPE: PRT
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APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
FULE REPERENCE: 600-1-253
CURRENT APPLICATION VINBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEO ID NOS: 43
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APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvach, Curt M
APPLICANT: Horvach, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INVERFACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
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5.5e-45;
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100.0%; Score 477; Di
Best Local Similarity 100.0%; Pred. No. 5.5s
Matches 95; Conservative 0; Mismatches
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; Sequence 16, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
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  SOFTWARE: Patentin Ver. 2.0
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; ORGANISM: Mus musculus
US-09-387-418A-17
                                                                                               ) ORGANISM: Mus musculus
US-09-387-418A-20
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SEQ ID NO 17
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SEQ ID NO 16
LENGTH: 176
                                                     LENGTH: 128
TYPE: PRT
                          SEQ ID NO 20
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0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 95; Conservative 0; Mismatches 0;
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Pred. No. 1.1e-44;
                                                                                                          61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
                                                                                                                                                                                                                                                                                  APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Cutr M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REPERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
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APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDEN
TITLE OF INVENTION: INTERACTIONS
                                                                                                                                                                                                                                   Sequence 29, Application US/09387418A Patent No. 6391572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-387-418A-30
; Sequence 30, Application US/09387418A
; Patent No. 6391572
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Best Local Similarity 100.0%;
Matches 95; Conservative 0;
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER SOFTWARE: Pate SEQ ID NO 29
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LENGTH: 229
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APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 229
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                                                                                                                 1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
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Pred. No. 1.1e-44;
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             Query Match
100.0%; Score 477; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 95; Conservative 0; Mismatches 0;
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Pred. No. 1.1e-44;
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Best Local Similarity 100.
Matches 95; Conservative
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US-09-387-418A-28
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SEQ ID NO 18
LENGTH: 229
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IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
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100.0%; Pred. No. 1.3e-44;
ive 0; Mismatches 0;
                          109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
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100.0%; Pred. No. 1.4e-44;
tive 0; Mismatches 0;
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APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvach, Curt M
APPLICANT: Darnell Jr. James E
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
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APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curk
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
    61 RSIVSELAGLLSAMEYVQKTLTDEELAD
                                                                                                                                            ; Sequence 14, Application US/09387418A; Patent No. 6391572; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 95; Conservative
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ORGANISM: Mus musculus
US-09-387-418A-14
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SOFTWARE: Pate
SEQ ID NO 14
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SEQ ID NO 9
LENGTH: 271
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Patent No. 6391572

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Zhang, Xiaokui
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 15
                                                                                                                                                                                               Sequence 31. Application US/09387418A
Patent No. 6391572
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Alang, Xiaokui
APPLICANT: Wizesczynska, Melissa H
APPLICANT: Horveth, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: NUMBER OS FOR 1059/387,418A
CURRENT APPLICATION UNMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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ive 0; Mismatches
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Db 215 RSIVSELAGLISAMEYVQKTLTDEELADWKRRPEI 249
Search completed: May 25, 2005, 17:47:37
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61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95

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| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-090-185-20
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Maximum Match 100%
Listing first 45 summaries
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No.
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Sequence 21, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wizeszzynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: MTREACTIONS
; TITLE OF INVENTION: UNPERF. US/10/090,185
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
LENGTH: 95
                                  Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 129, Appli
Sequence 149, Appli
Sequence 149, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 137, Appli
Sequence 139, Appli
Sequence 6, Appli
Sequence 7, Appli
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Sequence 19, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 16, Appli
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Sequence 6, 1
Sequence 5, 1
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US-10-090-185-9
US-10-639-6173-12
US-10-639-6173-12
US-10-380-020-4
US-10-380-020-5
US-10-380-020-5
US-10-380-020-5
US-10-380-020-5
US-10-380-020-5
US-10-117-087-2
US-09-925-302-780
US-09-925-302-780
US-09-925-302-780
US-09-925-302-780
US-09-925-302-780
US-09-925-302-780
US-09-925-302-780
US-10-177-293-439
US-10-755-889-362
US-09-833-205-6
US-09-876-773-8
US-10-639-617-8
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                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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; ORGANISM: Mus musculus
US-10-090-185-21
  JS-10-090-185-21
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Length 95 Indels

th 100.0%; Score 477; DB 13; Similarity 100.0%; Pred. No. 1.8e-42; 95; Conservative 0; Mismatches 0;

Query Match Best Local S Matches 95

9 9

1 VQDLEQKAKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR

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RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI

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US-10-090-185-19

Sequence 19, Application US/10090185

Sequence 19, Application No. US20020197647A1

Sequence 19, Application No. US20020197647A1

Sequence 19, Application No. US20020197647A1

APPLICANT: Areasy Xiaokui

APPLICANT: Mareaszaynaka, Melissa H

APPLICANT: Horvath, Curt M

APPLICANT: Horvath, Curt M

APPLICANT: Darnell Jr., James E

TITLE OF INVENTION: INTERACTIONS

FILE REFERENCE: 600-1-253

CURRENT APPLICATION NUMBER: US/10/090,185

CURRENT APPLICATION NUMBER: 09/387,418

PRIOR APPLICATION NUMBER: 09/387,418

PRIOR FILING DATE: 1999-08-31

WUMBER OF SEQ ID NOS: 43

SEQ ID NO 19

SED ID NO 19
                                                                                                                                                                                                                    IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
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100.0%; Pred. No. 4.8e-42;
iive 0; Mismatches 0;
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     US-10-090-185-16

Sequence 16, Application US/10090185

Publication No. US20020197647A1

GENERAL INFORMATION:

APPLICANT: Zhang, Xiaokui

APPLICANT: Wrzeszczynska, Melissa H

APPLICANT: Wanes E

TITLE OF INVENTION: INTERACTIONS

FILE REFERENCE: 600-1-253

CURRENT APPLICATION NUMBER: US/10/090,185

CURRENT FILING DATE: 2002-03-04

PRIOR PRILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN Ver. 2.0
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95; Conservative
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ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBLICANT: Zhang, Xiaokui APPLICANT: Zhang, Xiaokui APPLICANT: Zhang, Xiaokui Melissa H APPLICANT: Presezynska, Melissa H APPLICANT: Wrzeszczynska, Melissa H APPLICANT: Horvath, Cutr M APPLICANT: Darnell Jr., James B TITLE OF INVENTION: METHODS POR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR F TITLE OF INVENTION: INTERACTIONS FILE REFERENCE: 600-1-253 FILE REFERENCE: 600-1-253 CURRENT APPLICATION NUMBER: US/10/090,185 CURRENT PILING DATE: 2002-03-04 PRIOR FILING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 43 SOFTWARE: Patentin Ver. 2.0
                                                                                      APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REPERBACE: 600-1-253
CURRENT FILING DATE: 2002-03-04
PRIOR RPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SEQ ID NOS: 43
SEQ ID NO 20
LENGTH: 128
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2.6e-42;
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Best Local Similarity 100.0%; Pred. No. 2.6
Matches 95; Conservative 0; Mismatches
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Publication No. US20020197647A1
               Sequence 20, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus musculus US-10-090-185-20
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US-10-090-185-20
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Sequence 28, Application US/10090185
Publication No. US2020197647A1
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wizeszzynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: HORVATION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
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APPLICANT: Wzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Uzur Merensel
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION INVERSE: US/10/090,185
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 1999-04-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 229
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; ORGANISM: Mus musculus
US-10-090-185-28
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ORGANISM: Mus musculus
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Best Local Similarity
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Seque
                                                                                                                                                                                                                                                                            APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curr M
APPLICANT: Horvath, Curr M
APPLICANT: BARBAIJ Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE OF INVENTION: INTERACTIONS
FILE OF INVENTION: INVERSE: US/10/090,185
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 1999-08-31
NUMBER: OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 60
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86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                          Sequence 22, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 100.0
Best Local Similarity 100.0
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Best Local Similarity 100.
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mus musculus
US-10-090-185-22
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US-10-090-185-18
                                                                                                                                            -10-090-185-22
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US-10-090-185-14

i Sequence 14, Application US/10090185

j Publication No. US20020197647A1

j GENERAL INFORMATION:

j APPLICANT: Talong, Xiaokui

j APPLICANT: Mrzeszczynska, Melissa H

APPLICANT: Marzeszczynska, Melissa H

FILE NATION: MINERACTIONS

TITLE OF INVENTION: MINERACTIONS

FILE REFERENCE: 600-1-253

CURRENT PILING DATE: 2002-03-04

FRICR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFUMARE: PatentIn Ver. 2.0
                                                                                                                                                           WS-10-090-185-15
Sequence 15, Application US/10090185
Sequence 15, Application US/10090185
Sequence 15, Application No. US20020197647A1
Sequence 15, Application No. US20020197647A1
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Arzeszozynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: HORVATION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 477; DB 13; Best Local Similarity 100.0%; Pred. No. 5.5e-42; Matches 95; Conservative 0; Mismatches 0;
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                                             61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
                61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 236
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ORGANISM: Mus musculus
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US-10-090-185-15
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; Sequence 31. Application US/20020197647A1
; Sequence 31. Application No. US20020197647A1
; CENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR F
; TITLE OF INVENTION: INTERACTIONS
; TITLE OF INVENTION: INTERACTIONS
; TITLE OF INVENTION: UNMERR: US/10/090,185
; CURRENT FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR PLILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NOS: 43
; SEQ ID NOS: 43
; SED ID NOS: 2.0
                                                                                                                                                        Sequence 30, Application US/10090185
; Publication No. US20020197647A1
; Sequence 30, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INPORMATION:
APPLICANT: Wizeezczynska, Melissa H
APPLICANT: Wiree E
APPLICANT: Wiree E
APPLICANT: Wiree E
APPLICATION: WIREER: US/10/090,185
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 229
LENGTH: 229
TYPE: PRT
CORGANISM: Mus musculus
US-10-090-185-30
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100.0%; Pred. No. 5.3e-42;
iive 0; Mismatches 0;
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100.0%; Score 477; DB 13;
Best Local Similarity 100.0%; Pred. No. 5.3e-42;
Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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Matches 95; Conservative
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                                                                                                                        RESULT 10
US-10-090-185-30
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155 VQDLEQKWKVVENLQDDFDFDYXKTLKSQGDMQDLNGNNQSVTRQKWQQLEQMLTALDQMR 214
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                                                                                                   FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: US 08/126,589
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 477; DB 11;
Best Local Similarity 100.0%; Pred. No. 2.4e-41;
Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI 95
                                                                                APPLICATION NUMBER: US 07/980,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: May 25, 2005, 18:21:48
Job time : 53.9371 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS
          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELEX: 133521
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APPLICANT: Arzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REPERENCE: 600-11-253
FILE REPERENCE: 600-11-253
CURRENT APPLICATION UNMBER: US/10/090,185
CURRENT APPLICATION NUMBER: 09/387,418
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999.08-31
49 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 271;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                   109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
                                                     61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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100.0%; Score 477; Dest Local Similarity 100.0%; Pred. No. 6.5
Matches 95; Conservative 0; Mismatches
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APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
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ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09876773
Publication No. US20040058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
                                                                                                                                                                                                                                 Sequence 9, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
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STATE: New Jersey
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SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                   RESULT 14
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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•	RESULT 1 A5444 DNA-binding protein APRF - human C; Species: Homo sapiens (man) C; Date: 21-Feb-1997 #sequence_revision 21 C; Date: 21-Feb-1997 #sequence_revision 21 C; Accession: A5444 A; Title: Molecular cloning of APRF, a nov-A; Title: Molecular cloning of APRF, a nov-A; A; Accession: A54444 A; Accession: A54444 A; Accession: A54444 A; Molecule type: mANA A; Molecule type: mANA A; Residues: 1-770 cRES A; Cross-references: UNIPROT: P40763; GB:L2 A; Cross-references: UNIPROT: P40763; GB:L2	ng prote : Homo E 1-Feb-19 on: A544 63.7 N18: 63.71, 1 Molecula ce numbe on: A544 prelimi e type: 8: 1-770	protein APRF como sapiens eb-1997 #seq A54444 Nishio, Y.; 71, 1994 number: A5444 A54444 A5444 A54444 A5444 A5444 A5444 A5444 A5444 A5444 A544 A5444 A5	F - human (man) quence_re ; Inoue, ing of AP 444; MUID translate	man _rev e, h APF UID: atec		change 09-Jul-; // Matsusaka, T.; ted gene factor: 788; PID:g475789	2004 Yoshida, K.; Su 3 p91-related tr
	A,Gene: GDB:STAT3; APRF A,Cross-references: GDB:358950 A,Map position: 17q21-17q21 C,Superfamily: human signal tr C,Keywords: DNA binding; trans	D:STAT3 eference ition: 1 mily: hu	APRE Se: GDB 7q21-1 Iman si	:35895 7 <u>q</u> 21 gnal t ; tran	0 rang scri	er and on fact	transcription activator STAT5A or	4
	Query Match Best Local (Matches 9	(A W	97. Jarity 97. Conservative LEQKMKVVENLQ	97. 97. vative VVENLQ	97.7%; 97.9%; ive	Score 466; DB 2; Pred. No. 1.3e-31 1; Mismatches	97.7%; Score 466; DB 2; Length 770; imilarity 97.9%; Pred. No. 1.3e-31; ; Conservative 1; Mismatches 1; Indels 0; Gaps VQDLEQXMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR	в 0; МR 60
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1930's pol-related transcription factor - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (C.5pecies: Mus musculus (house mouse) (C.5pecies: Mus musculus (house mouse) (C.5pace: 0.2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004 (C.5Accession: 149508) 149009 (C.5Accession: 149508 (C.5Accession: 149508 (C.5Accession: 15944) (MulD: 94208062; PMID: 7512451 (C.5Accession: 149508 (C.5Accessio

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A,Cross-references: UNIPROT:P42232; UNIPROT:Q9JKM1; EMBL:U21110; NID:g747973; PIDN:AACS R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A. Bakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A. A. H., 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin A;Reference number: S54772; MUID:95237198; PMID:7720707
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A; Cross-references: EMBL: Z48539; NID: g758635; PIDN: CAA88420.1; PID: g758636
A; Cross-references: EMBL: Z48539; NID: g758635; PIDN: CAA88420.1; PID: g758636
R; Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris, BRBO J. 14, 1402-1411, 1995
A; Title: Interleukin-3 signals through multiple isoforms of Stat5.
A; Reference number: S54725; MUID: 95246733; PMID: 7537213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NiAlternate names: STATS protein homolog p80
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149274; S54773; S54773; S54727
R;Liu, X.; Robinson, G.W.; Goulleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8813-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved
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NiAlternate names: stat5 protein
CiSpecies: Mu musculus (house mouse)
CiSpecies: Mu musculus (house mouse)
CiSpecies: Mu musculus (house mouse)
CiAccession: S$4773, 149273
R;Mui, A.L.F.; Wakao, H; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
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C;Superfamily: human signal transducer and transcription activator STAT5A
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                       33.1%; Score 158; DB 2; 36.2%; Pred. No. 8.9e-06; iive 22; Mismatches 36,
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A,Molecule type: mRNA
A,Residues: 1-432,'E',434-786 <AZA>
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A; Residues: 1-786 < RES>
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R; Yamamorto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, R; Yamamorto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, Mol. Cell. Biol. 14, 432-4349, 1994

A; Pitle: Stat4, a novel gamma interferon activation site-binding protein expressed in ea A; Reference number: A56047, MUID:94277038; PMID:8007943

A; Accession: A56047

A; Accession: A56047

A; Residue: preliminary; nucleic acid sequence not shown A; Molecule type: mRNA

A; Residues: 1-748 extANA

A; Cross-references: UNIPROOT:P42228; GB:U09351; NID:9509502; PIDN:AAA19692.1; PID:9509503

C; Superfamily: human signal transducer and transcription activator STATSA

C; Keywords: DNA binding; phosphoprotein
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Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A,Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa ISGA,Reference number: A46159; MUID:92366557; PMID:1502203
A,Title: Acute phase response factor and additional members of the interferon-stimulated
A;Reference number: 149009, MUID:95014185, PMID:7523373
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C;Date: 19-Oct_1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
                                                                    A;Accession: 149009
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Ataus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-393, M',395-700,702-770 <RE2>
A;Residues: 1-393, M',395-700,702-770 <RE2>
A;Cross-references: EMBL:U08378; NID:g473889; PIDN:AAA56668.1; PID:g473890
C;Genetics: ApRF
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.4%; Score 164; DB 2; Length 748; 35.1%; Pred. No. 2.8e-06; Live 26; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                  Length 770;
                                                                                                                                                                                                                                                                                                                                                              Match 97.7%; Score 466; DB 2; Length 77 Local Similarity 97.9%; Pred. No. 1.3e-31; Length 77 les 93; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 MRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: nucleic acid; protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: UNIPROT:P42224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Experimental source: HeLa cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 35.1%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -739 <SCH>
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48; Indels

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A.Cross-references: UNIPROT: P42231; EMBL:X78428; NID:g602354; PIDN:CAA55191.1; PID:g602 A;Note: this is a revision to the sequence from reference S44353 K;Natao, H.; Gouilleux, F.; Groner, B. EMBO J. 13, 2182-2191, 1994
A;Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcr A;Reference number: S44353; MUID:94244619; PMID:7514531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Best Local Similarity
            A; Molecule type: mRNA
A; Residues: 1-794 < WAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-533 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: G72593
A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                A;Accession: S44353
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A;Gene: APE1216
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S33124
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                                                                                                     A; Accession: S3.7, And A; Accession: S1.7, A; Accession: L1.793 A; Acce
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submitted to the EMBL Data Library, December 1995

submitted to the EMBL Data Library, December 1995

A.Reference number: H01043

A.Recession: G02317

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Residues: 1-794 < LLIN-

A.Residues: 1-794 < LLIN-

A.Cross-references: UNIPROT: P42229; EMBL: U43185; NID: g1151169; PIDN: AAB06589.1; PID: g115

C.Superfamily: human signal transducer and transcription activator STATSA
:Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
Reference number: S54772; MUID:95237198; PMID:7720707
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R;Wakao, H.; Gouilleux, F.; Groner, B.
BMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regula
A;Reference number: S55527; MUID:95188889; PMID:7882987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ښ</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Homo sapiens (man)
Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
Accession: G02317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ODLEQKMKVVENLQDDFDFNY-KTLKSQGDMQDLNGNN-----QSVTRQKMQQLEQML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 QREAQTLQQYRVELAEKHQKTLQLLRKQQTIILDDELIQWKRRQQL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 QREAQTLQQYRVELAEKHQKTLQLLRKQQTIILDDELIQWKRRQQL 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 793; 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
19.5%; Score 93; DB 3
Best Local Similarity 26.4%; Pred. No. 2.7;
Matches 28; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription activator stat5A - human
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Matches 27; Conservative
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C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72593
C;Accession: G72593
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
A)R Res. G, 83-101, 1999
A;Ritle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q9YCP2; DDBJ:AP000061; NID:g5104821; PIDN:BAA80205.1; PID:d
A;Experimental source: strain K1
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S33124; S23740; S00928; G01185
R;Mitchell, P.J.; Cooper, C.S.
Oncogene 7, 2329-2333, 1992
A;Title: The human tpr gene encodes a protein of 2094 amino acids that has extensive co
A;Reference number: S33124; MUID:93064711; PMID:1437155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: kinase-related transforming protein (tpr-met); protein with promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 QDTENELKKLQQTQEYFIIQYQESLRIQAQFAQLAQLNPQERLSRETALQQKQVSLEAWL 216
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A;Molecule type: mRNA
A;Residues: 1-716, RHLHGPGSLPSR',729,'P',731,'ASL' <WAW>
A;Cross-references: EMBL:X78428
A;Note: this sequence has been revised in reference S55527
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                              12;
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                                                                                                                                                                                                                               DB 2; Length 533;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 QREAQTLQQYRVELAEKHQKTLQLLRKQQTIILDDELIQWKRR 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 A-STLQQLQQRLATAEESLQALTEDLASLQAEVETLQQSIVE 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 TROKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein APE1216 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 ----TALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 18.0%; Score 86; DB;
1. Similarity 22.5%; Pred. No. 6.9;
23; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VQDLEQKMKVVEN----LQDDF----
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A;Cross-references: UNIPROT:P45970; EMBL:Z36753; PIDN:CAA85342.1; GSPDB:GN00020; CESP:T'
A;Experimental source: clone T09A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364K Golgi complex-associated protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession. JC5837
R;Toki, C.; Fujiwara, T.; Sohda, M.; Hong, H.S.; Misumi, Y.; Ikehara, Y.
Cell Struct. Funct. 22, 565-577, 1997
A;Title: Identification and characterization of rat 364-kDa Golgi-associated protein re-
A;Reference number: JC5837; MuID:98093490; PMID:9431462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-3187 <TOK>
A;Cross-references: UNIPROT:Q63714; DDBJ:D25543; NID:g516825; PIDN:BAA05026.1; PID:g516
C;Comment: This protein plays a role in the formation and maintenance of the characteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Superfamily: glantin
F,49-549,624-1176,1238-1707,1763-3114/Domain: coiled-coil leucine zipper #status predic
F,3165-3187/Domain: membrane anchor #status predicted <MAD>
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------NNOSVIROKMO 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein T09A5.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T24728 R;Lightning, J. Species: Caenore number: 21928 A;Reference number: 21928 A;Reference number: 21928 A;Accession: T24728 A;Access
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 DLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQ----
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Best Local Similarity 23.9%; Pred. No. 15;
Matches 27; Conservative 22; Mismatches 31; Indels 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 ------MRRSIVSE---LAGLLSAMEYVQKTLTDEE 85
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                                                                                                                                                           60 RRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
132 LEELKRKVRRLEVLEDDFDHLKEQLIKQEGQLE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 OLEOMLTALDOMRRSIVSELAGLLSAMEYV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Map position: 2
A,Introns: 47/2; 253/2; 604/3; 643/1; 712/3
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                                                        A; Residues: 1-2094 - MIT>
A; Cross-references: UNIPROT:015624; UNIPROT:09UE33; EMBL:X66397; NID:9633225
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
R; Mitchell, P.J.; Cooper, C.S.
A; Title: Nucleotide sequence analysis of human tpr cDNA clones.
A; Received on number: $23740; MUID:92195670; PMID:1549355
A; Residues: 223740
A; Residues: Drellminary
A; Molecule type: mRNA
A; Residues: 1-725, LV - MIZ>
A; Residues: 1-725, LV - MIZ>
A; Residues: 1-725, LV - MIZ>
A; Residues: 2, 617-619, 1988
A; King, H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J.
Oncogene 2, 617-619, 1988
A; Title: Tpr homologues activate met and raf.
A; Reference number: $00928; MUID:88262257; PMID:3387099
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A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB2166
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G75219
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome A;Reference number: A75001
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                    A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 144-228 «GRE>
A,Gross-references: EMBL:X94208; NID:g1296797; PIDN:CAA63904.1; PID:g1296798
C,Genetics:
A,Gene: GDB:TPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: mRNA
Residues: 1-31,'R',33-142 <KIN>
Cross-references: EMBL:Y00672; NID:g37255; PIDN:CAA68681.1; PID:g37256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, December 1995
A;Reference number: H00592
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17.9%; Score 85.5; DE
Best Local Similarity 26.5%; Pred. No. 33;
Matches 26; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 DLEQKMKV---VENLODDFDFNYKTLKSQ---
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A;Map position: 1q25-1q25
A;Introns: 177/3
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A,Molecule type: DNA
A,Residues: 1-217 <KAW>
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Best Local &
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1 VQDLEQKWKVVENLQDDFD-FNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQM 59

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R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae A;Reference number: S73327; MUID:97105885; PMID:8948633
                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1818 <HIM>
A;Residues: 1-1818 <HIM>
A;Cross-references: UNIPROT:P75471; EMBL:AE000051; GB:U00089; NID:g1674211; PIDN:AAB9617
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:059525; GB:AP000007; NID:g3236134; PIDN:BAA31017.1; PID:g325
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
A;Gene: PH1895
protein MG218 homolog F10_orf1818 - Mycoplasma pneumoniae (strain ATCC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekii M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch) MA. Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1291 VSELROEKKOLLSAGKQVDDKSRLLEQNORHLONLS----SETKKKROSLEHDINKFDOR 1346
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                  10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Pyrococcus horikoshii
.Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1818;
                                                                                                                                                                                                                                                                                                                                                                                                                        C,Genetics:
A,Genetic code: SGC3
C,Superfamily: Mycoplasma genitalium hypothetical protein MG218
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Job time : 12.9623 secs
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Best Local Similarity 27.5%;
Matches 28; Conservative 2
                             Species: Mycoplasma pneumoniae
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Best Local Similarity
Matches 20; Conserv
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Perfect score:

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TISSUE=Kidney, and Pancreas;

TISSUE=Kidney, and Pancreas;

X MEDINE=21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blate N.K.,

A Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernath K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Placenta;
MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,
Yoshida K., Sudo T., Naruto M., Kishimoto T.;
"Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
related transcription factor involved in the gp130-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.
Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
Rajkumar N., Yi Q., Nickerson D.A.;
"SeattleSNPs. NHLBI H46682 program for genomic applications, UW-
FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;
"Highly conserved amino-acid sequence between murine STAT3 and a
Gene 213:119-124(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      response factor).
Name-STATJ; Synonyms-APRF;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STA3_HUMAN STANDARD; PRT; 770 AA.
P40763; O14916; Q9BW54;
O1-FEB-1995 (Rel. 31, Created)
05-JUL-2004 (Rel. 4F). Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase
P42224
068d00
08jfu8
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07zz77
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013131
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08jf85
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STA1 HUMAN
Q68BD0
Q8ABD0
Q8JFUB
Q8JFUB
Q7ZZ53
Q8AW20
Q7ZZ73
Q8JFU7
Q13131
Q6P943
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Q66hb2
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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STA3_MOUSE
STA3_RAT
STA3_BOVIN
Q6DV79
Q704W6
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Q90Y16
STA4 HUMAN
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Q8C3V4
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Maximum Match 100%
Listing first 45 summaries
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Q7 ZXK3
Q6 DVF3
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Q6 NV4 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                 US-10-090-185-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
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Match Length
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0005737; C:cytoplasm; TAS.
GO:0005634; C:nucleus; TAS.
GO:0005662; F:hematopoietin/interferon-class (D200-domain. ..; TAS.
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COGGLIVATOR WORN, SALES, 9, 10 Biol. Chem. 277:8004-8011(2002).

1- FUNCTION: Transcription factor that binds to the interleukin-6

1- FUNCTION: Transcription factor that binds to the interleukin-6

1- FUNCTION: Transcription factor that binds to the promoters of various (L.6) -reapponaive elements identified in the promoters of various acute-phase protein genes.

1- FATHWAY: Involved in the gp130-mediated signaling pathway.

1- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAYI). Interacts with NCOA1.

1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.

1- ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolda-P40763-2; Sequence-VSP 010474;
Isolda-P40763-2; Sequence-VSP 010474;
TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas.
PIN: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, IIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity.
SIMILARITY: Belongs to the transcriptional activity.
SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11773079; DOI=10.1074/jbc.M111486200;
Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
"Functional interaction of STAT3 transcription factor with the
coactivator NGA/SRCIa.";
                                                                                                                                                                                                                                                                                                                             MEDLINE-95215843; PubMed-7701321;
Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
"Requirement of serine phosphorylation for formation of STAT-promoter
                                                                                                                                                                                                                                                ·.
                                                                                                                                                                                                                                                Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isold=P40763-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ012463; CAA10032.1; -. EMBL; AY572796; AAS65886.1; -. EMBL; BC000627.1; -. EMBL; BC014482; AAH14482.1; -. EMBL; AF029311; AAB84254.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L29277; AAA58374.1; -.
                                                                                                                                                                                                         SEQUENCE OF 564-704 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            Science 267:1990-1994 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P42227; 1BG1.
TRANSFAC; T01493; -.
Genew, HGNC:11364; STAT3.
                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION ON SERINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H-InvDB; HIX0013840; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH NCOAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A54444; A54444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Del-701
                                                                                                                                                                                                                                  TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102582;
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VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 60
                                        . .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/C; TISSUE=Liver;
MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
Yoshida K., Sudo T., Naruto M., Kishimoto T.;
"Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
related transcription factor involved in the gpl30-mediated signaling
                                                                                                                                                                                                                                Phosphotyrosine (by JAK) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
AND 632-640.
                                                                                                                        PFEAM; PF00017; SH2; 1.

PFEAM; PF01017; SH2; 1.

PFEAM; PF02864; STAT_bind; 1.

PROSITE; PS50001; SH2; 1.

PROSITE; PS50001; SH2; 1.

Activator; Alternative splicing; DNA-binding; Nuclear protein; Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.

DOMAIN SH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mus musculus (mouse).
Sakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
 GO, GO:0003700; F:transcription factor activity; TAS.
GO; GO:0006928; P:cell motility; TAS.
GO; GO:000122; P:dAK-STAT cascade; TAS.
GO; GO:0000122; P:neqative regulation of transcription from P.
GO; GO:0007399; P:neurogenesis; TAS.
GO; GO:0007399; P:signal transduction; TAS.
InterPro; IPR009867; PS3_like_DNA_bnd.
InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 1; Length 770; 2.4e-31;
                                                                                                                                                                                                                                          Phosphoserine (By smilarity)
Missing (in isoform Del-701).
/Fride_VSp_010474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                          Q -> H (in Ref. 1).
P -> S (in Ref. 1).
K -> N (in Ref. 1).
F -> Y (in Ref. 1).
V -> L (in Ref. 1).
T -> A (in Ref. 1).
T -> A (in Ref. 1).
W, 6C00632211C8012D CRC64;
                                                                                                                                                                                                                                                                                        0 -> K (in dbSNP:1803125)
GO:0003700; F:transcription factor activity; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
                                                                                                                                                                                                                                                                                                      FTIG=VAR_018683
                                                                                                                                                                                                                                                                                                                                 FTIG=VAR_018679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               770 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.7%; Score 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEOUENCE FROM N.A. (ISOFORM STAT3A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                88067 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity 97.9%;
93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Stat3; Synonyms=Aprf;
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                                                                                                                                                                                                                                                                                                                                                             460
548
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727
701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 77:63-71(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                770 AA;
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                                                                                                                                                                                                                            580
705
727
701
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667
730
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P42227;
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CONFLICT
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SEQUENCE
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MOD_RES
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Best Local
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SEQUENCE FROM N.A. (ISOFORM STAT3A).

STRAIN=FVEN, TISSUE-Mammary gland;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altechul S.F., Zeeberg B., Buetow K.H., Schmeen C.M., Schuler G.D.,

Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roder A., Schein J.E., Jones S.J.M., Marra M.A.,

Rader A., Schein J.E., Jones B.J.M., Marra M.A.,

Rader A., Schein J.E., J., Shalska U., Smailus D.E.,

Rader A., Schein J., Schein J.E., Jones B.J.M., Marra M.A.,

Rader A., Schein J., Schein J.E., Jones B.J.M., Marra M.A.,

Rader A., Schein J., Schein 
                                                                                                                                                                                                                                              MEDLINE=95014185; PubMed=7523373;
Raz R., Durbin J.E., Levy D.E.;
"Acute phase response factor and additional members of the interferon-stimulated gene factor 3 family integrate diverse signals from cytokines, interferons, and growth factors.";
J. Biol. Chem. 269:24391-24395(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.

MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
Wen Z., Zhong Z., Darnell J.E. Jr.;
"Maximal activation of transcription by Statl and Stat3 requires both tyrosine and serine phosphorylation.";
Cell 82:241-250(1995).
                                                 Zhong Z., Wen Z., Darnell J.E. Jř.;
"Stafa: a STAT family member activated by tyrosine phosphorylation in response to epidermal growth factor and interleukin-6.";
Science 264:95-98(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11161808; DOI=10.1006/geno.2000.6413;
Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T.,
Dewar K., Hennighausen L.;
"Structure of the mouse stat 3/5 locus: evolution from Drosophila to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schaefer T.S., Sanders L.K., Nathans D.; "Cooperative transcriptional activity of Jun and Stat3 beta, a short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J, and NOD/LtJ;
Davoodi-Semiromi A., She J.-X.;
A mutant StatSb with weaker DNA binding defines a key defective pathway in non-obese diabetic (NOD) mice.";
Submitted (WAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM STAT3B).
STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
MEDLINE=96016116; PubMed=7568080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM STAT3A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM STAT3A).
                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM STAT3A).
                               MEDLINE=94188718; PubMed=8140422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 71:150-155(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zebrafish to mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stat3."
TISSUE=Thymus;
                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              form of
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EMBL; 129278; AAA19254.1; -
DR EMBL; 106922; AAA19452.1; -
DR EMBL; 1006922; AAA19452.1; -
DR EMBL; 1006922; AAA19452.1; -
DR EMBL; 408378; AAA52612.1; -
DR EMBL; AV299489; AAA75418.1; -
DR EMBL; AV29489; AAA75418.1; -
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
GO; GO:0007559; P:JAK-STAT cascade; IDA.
Therefore, TDD006667; DR3 11'e num hund from Pol II pro. .; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphotyrosine (by JAK) (By similarity).
                                                       Nature 394:145-151(1998).

-! FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6) responsive elements identified in the promoters of various acute-phase protein genes. STAT3B interacts with the N-terminal part of JUN to activate such promoters in a cooperative way.
-! PATHWAY: Involved in the gp130-mediated signaling pathway.
-! SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).
-! SUBCELLUIAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                       Name=bel-701;
ISOUE-842227-3; Sequence=VSP 010475;
ISOUE-842227-3; Sequence=VSP 010475;
TISSUE SPECIFICITY: STAT3A is geen in the liver, although in a much kidney. STAT3B is also detected in the liver, although in a much less abundant manner.

PTW: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, ILF, GSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity (By similarity). SIMILARITY: Belongs to the transcription factor STAT family.
Becker S., Groner B., Mueller C.W.; "Three-dimensional structure of the Stat3beta homodimer bound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IRR000867; PS3 like DNA_bnd.
InterPro; IRR000867; PS3 like DNA_bnd.
InterPro; IRR000807; STAT.
InterPro; IRR00017; STAT.
Pfam; PRO1017; STAT alpha; 1.
Pfam; PRO2064; STAT bind; 1.
PROSITE; PS50001; SHZ; 1.
PROSITE; PS50001; SHZ; 1.
Direct protein sequencing; DNA-binding; Nuclear protein;
Phosphorylation; SHZ domain; Transcription regulation.
                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphoserine.
                                                                                                                                                                                                                                                                                                                                                                 Name=Stat3B;
IsoId=P42227-2; Sequence=VSP_006287;
                                                                                                                                                                                                                                                                                                                                         IsoId=P42227-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                           Name=Stat3A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD RES
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                                            DNA.";
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response to phosphorylation (By similarity)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Transcription factors Stat3 and Stat5b are present in rat liver nuclei late in an acute phase response and bind interleukin-6 response
ITCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 270:29998-30006(1995).

-! FUNCTION: Transcription factor that binds to the interleukin-6

(IL-6)-responsive elements identified in the promoters of various
acute-phase protein genes.

-! PATHWAY: Involved in the gp130-mediated signaling pathway.
-! PATHWAY: Forms a homodimer or a heterodimmer with a related family member (at least STATI). Interacts with NCOA1 (By similarity).
-! SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                     1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
           FDMDLTSECATSPM -> FIDAVWK (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.2998; Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F., Fey G.H.;
                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                 /FTId=VSP_006287.
Missing (in isoform Del-701).
/FTId=VSP_010475.
S->A: Decreased transcriptional
                                                                                                                                                                                                                                                                                                                                                                     97.7%; Score 466; DB 1; Length 770; 97.9%; Pred. No. 2.4e-31;
                                                                                             E -> K (in Ref. 2).
S -> T (in Ref. 2 and 4).
M -> I (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        770 AA
                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.4e
1; Mismatches
                                                                                    activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                      727
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
ses 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                              16
133944
11394
11394
1181
1181
1181
1282
1382
1393
1302
1330
1330
1330
                                                                       727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Stat3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elements."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STA3 RAT
P52631;
                                                                                              CONFLICT
CONFLICT
CONFLICT
HELIX
                                                                                                                                                                                                                                                                                                                                                                        Query Match
VARSPLIC
                                                /ARSPLIC
                                                                       AUTAGEN
                                                                                                                                                        TURN
HELIX
TURN
HELIX
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HELIX
TURN
HELIX
                                                                                                                                                                                                                                                                                                                      STRAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUB=Mammaly gland;
Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various acute-phase protein genes (By similarity).
-!- PATHWAY: Involved in the gp130-mediated signaling pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
           PTM: Tyrosine phosphorylated in response to fir-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity (By similarity). SIMILARITY: Belongs to the transcription factor STAT family. SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
MCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphotyrosine (by JAK) (By
Phosphoserine (By similarity)
D74A0C76954754ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (Rel. 44, Created)
5-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.7%; Score 466; DB 1;
97.9%; Pred. No. 2.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               770 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                 HSSP; P42227; 1BG1.
RGD; 3772; Stat3.
InterPro; IPR009967; P53_like_DNA_bnd.
InterPro; IPR0009967; P53_like_DNA_bnd.
InterPro; IPR001217; STAT.
Pfam; PP01017; STAT_alpha; 1.
Pfam; PP01017; STAT_alpha; 1.
Pfam; PP02865; STAT_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88039 MW;
                                                                                                                                                                                                                                                                                                 EMBL; X91810; CAA62920.1; -. HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [Similarity 97.9%; 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=STAT3;
Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match_
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STA3 BOVIN
P61635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
MOD_RES
SEQUENCE
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Matches
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DLEQKWKVVENLQDDFDFNYKTLKSQ-DMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Mammary gland;

Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;

Subject H.M., Wheeler T.T., Moolenaar A., Pitra C.;

R. Subject H.M., Moolena H. Subject H.M., Pitra C.;

R. Subject H.M., Moolena H.M., Pitra C.;

R. Subject H.M., Moolena H.M., Pitra C.;

R. Subject H.M., Moolena H.M., Pitra 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 DLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
BEDLINE-20107399, PubMed=10642787; DOI=10.1006/dbio.1999.9518;
Nishinakanura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
Asashima M., Yokota T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Signal transducer and activator of transcription 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.3%; Score 440.5; DB 2; Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                Pred. No. 4.1e-30;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 IVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
                                                                                                                      RSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               769 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90; Conservative
                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovinae; Bos
                                                                                                                                                                  215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=stat
                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stat 3.
                                                                                                                                                                                                                                                                               Q704W6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9PVX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Q9PVX8
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                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation (By similarity).
-!- SIMILARITY: Belongs to the transcription factor STAT family.
-!- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 VQDLEQKMKVVENLLDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhou G.Y., Leung F.C.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY641397, AAT64887.1;
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007370; F:transcription factor activity; IEA.
GO; GO:000735; P:transcription factor activity; IEA.
InterPro; IPR0098967; F33_like_DNA_bnd.
InterPro; IPR0098967; F33_like_DNA_bnd.
InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphotyrosine (by JAK) (By si
Phosphoserine (By similarity).
9CEB147C73E83274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.2%; Score 459; DB 1; Length 770; 96.8%; Pred. No. 9.4e-31; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.5%; Score 451; DB 2; Length 771;
94.7%; Pred. No. 4.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88174 MW; 71AC855C5DEC03E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal transducer and activator of transcription 3 Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           771 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       EMBL; AJ620655; CAF06182.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   770 AA; 87974 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF01017; STAT alpha; 1.
PF02864; STAT_bind; 1.
PF02865; STAT_int; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 96.8°
Matches 92, Conservative
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Matches 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00017; SH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
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MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6DVF3
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             임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
"Activation of Stat3 by cytokine receptor gpl30 ventralizes Xenopus embryos independent of BMP-4.";
Dev. 1516:481-490(1999).
EMBL; AB017701; BAA86061.1; -.
HSSP; P42227; 1861.
                                                                                                                                                              GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008867; PS3 like_DNA_bnd.
InterPro; IPR008967; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.6%; Score 432; DB 2; Length 769; 88.4%; Pred. No. 1.9e-28; ive 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87974 MW; 0905C03263303069 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF00017; SH2; 1.
Pfam, PF01017; STAT alpha; 1.
Pfam, PF02864; STAT bind; 1.
Pfam, PF02865; STAT_int; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
hes 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50001; SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      769 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00252; SH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=stat3-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                SO DE RELEASE DE LA PERSONA DE
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155 VQDLEQXAKXVENLQDDFDFNYKTLKSQSDLSELNGNNQSVTRQKMQQLEQMLTALDQLR 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0004871; F:signal transducer activity; IEA.

R GO; GO:0007242; P::ntraceclption factor activity; IEA.

R GO; GO:0007242; P::ntraceclption factor activity; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR0009967; PE3_like_DNA_bnd.

InterPro; IPR0009967; PE3_like_DNA_bnd.

R Pfam; PF00017; SH2T.

R Pfam; PF00017; SH2T alpha; 1.

R Pfam; PF02864; STAT alpha; 1.

R Pfam; PF02865; STAT lint; 1.

R SWART; SW00252; SH2; 1.

R PROSITE; PS50001; SH2; 1.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
SiOCT-2004 (TrEMBLrel. 28, Last annotation update)
Signal transducer and activation of transcription factor 3.
Oryzias latipes (Medaka fish) (Japanese ricefish).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
                                                                                                                     "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Length 766;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                TISSUE=Embryo;
Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO447171; AAH44717.1; -.
HSSP; P42227; 1BG1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     766 AA; 87599 MW; 31018A3321CCEB9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 427; DB 2;
Pred. No. 5e-28;
7; Mismatches
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Pfam; PF01017; STAT_alpha; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.5%;
                                                                                                                                                                                                          Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                            initiative.";
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Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                  Brachydanio rerio (Zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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Q6NV46
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                                                                                                                                   213
                                                                                                                     1 VQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDM-QDLNGNNQ-SVTRQKMQQLEQMLTALDQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLNGNNQ-SVTRQKMQQLEQMLTALDQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last amoctation update)
05-JUL-2004 (TrEMBLrel. 27, Last amoctation update)
05-JUL-2004 (TrEMBLrel. 27, Last amoctation and action and activator and activator of transcription 3 isoform 1.
07-yzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Orartebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Eloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu R., Hong Y.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AX641434, 2A146364.1;
GO, GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007402; P:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:000555; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; F93_like_DNA_bnd.
InterPro; IPR001217; STAT.
                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.9%; Score 381; DB 2; Length 785; Best Local Similarity 77.3%; Pred. No. 4.2e-24; Matches 75; Conservative 14; Mismatches 6; Indels
                                                                 79.9%; Score 381; DB 2; Length 765; 77.3%; Pred. No. 4.1e-24;
                                                                                           6; Indels
                                     765 AA; 87566 MW; F5D01408748EC703 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89643 MW; 81F231BDE27DE938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                      214 LRRQIVTEMGGLLIAMDYVQKNLTDEELADWKRRQQI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250
                                                                                                                                                                          95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI 95
                                                                                                                                                                       59 MRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|| ||:|: |||:||:||:|| ||||||||||||:|
LRRQIVTEMGGLLTAMDYVQKNLTDEELADWKRRQQI
                                                                                                                                                                                                                                                                     785 AA.
                                                                                ; Pred. No. 4.1e
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
PROSITE; PS5001; SH2; 1.
SEQUENCE 765 AA; 87566 MW
                                                                             Local Similarity 77.3%; tes 75; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   072TS5;
01-JUN-2003 (TEMBLTEL: 24,
01-JUN-2003 (TEMBLTEL: 24,
01-MAR-2004 (TEMBLTEL: 26,
                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50001; SHZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           785 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8090;
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                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                   Q6GUE7
                                                                                Best Loc
Matches
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TISSUB-Whole body;

KA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Brownstein M., Soares M.B., Bonaldo M.E., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Frange C.,

RA Brownstein M.J., Widin T.B., Tochhyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McEwan P.J., McKernan R.J., Mazk J.A., Gunaratne P.H.,

Robard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A rilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rhiting M. Naria M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Robersation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GG; GG:0005634; C:nucleus; IEA.
GG; GG:0004871; F:signal transducer activity; IEA.
GG; GG:000471; F:signal transducer activity; IEA.
GG; GG:0003700; F:transcription factor activity; IEA.
GG; GG:0006355; P:regulation of transcription, DNA-dependent; IEA.
GG; GG:0007165; P:signal transduction; IEA.
InterPro; IPR009967; PS] like_DNA_bnd.
InterPro; IPR001217; PSAT.
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
Straubberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC04527; AAH45276.1; -.
HSSP; P42227; 1BG1.
ZFIN; ZDB-GENE-980526-68; stat3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF01017; STAT_alpha; 1.
PF02864; STAT_bind; 1.
PF02865; STAT_int; 1.
NCE 414 AA; 48253 MW; 0FFD1B509B7526BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last sequence update)
Last annotation update)
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Brachydanio rerio (Zebrafish) (Danio rerio).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
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                                                                                                                                       A Strausberg K. L. Feingold E.A., Grouse L.H., Derge J.G.,

RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Richard R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alteshul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Alteshul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Alteshul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Boatleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robert S.A., McEwan P.J., McKernan K.J., Matek J.A., Gunaratne P.H.,

Richards S., McDewn P.J., McKernan R.J., Mark, Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahes S., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,

Whithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Jones S.J., Marra M.A.;

Yand Generation and initial analysis of more than 15,000 full-length human Meden Medel Mede
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004871; F:signal transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008867; P53_like_DNA_bnd.
InterPro; IPR009805; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC068320; AAH68320.1; -.
ZFIN; ZDB-GENE-980526-68; stat3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90039 MW; FC7371D0B0E5447E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
PROSITE; PS50001; SH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           786 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              roc. Natl. Acad.
                                                                                                                  SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=stat3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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              셤
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Brachydanio rerio (Zebrafish) (Danio rerio)

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1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLNGNNQ-SVTRQKMQQLEQMLTALDQ
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007242; F:stranscription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006352; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008967; P53_like_DNA_bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Butaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopeerygii; Teleostei; Buteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                         k; Score 379; DB 2; Length 806;
k; Pred. No. 6.4e-24;
14; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Johnson M.C., Mourich D.V., Leong J.C.;
Johnson M.C., Mourich D.V., Leong J.C.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U6033; AAB60926.1; -.
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT lint; 1.
SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;
                                                                                                                                                                                                                                                                                                                                                  92151 MW; 74BC4EA401C3C942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                  767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                               79.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 77.39 tes 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        806 AA;
                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                               1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-ODLNGNNQ-SVTRQXMQQLEQMLTALDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VQDLEQXMKVVENLQDDFDFNYKTLKSQGDM-QDLNGNNQ-SVTRQXMQQLEQMLTALDQ
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetraodontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
PFam; PF00017; SH2; 1.
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78.4%; Score 374; DB 2; Length 764;
Best Local Similarity 76.3%; Pred. No. 1.6e-23;
Matches 74; Conservative 14; Mismatches 7; Indels
      Length 767;
                                   Indels
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Submirted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307106; AAL09415.1; -.
HSSP; P42227; 18G1.
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87411 MW; E661FFE18BEFD8BE CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                               MRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI 95
Ouery Match 78.6%; Score 375; DB 2; L
Best Local Similarity 75.3%; Pred. No. 1.3e-23;
Matches 73; Conservative 17; Mismatches 5;
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Job time : 44.5283 secs
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regulation o.

rema; PF01017; SH2; 1.

R Pfam; PF02864; STAT alpha; 1.

R Pfam; PF02864; STAT alpha; 1.

R SMART; SM00252; SH2; 1.

PROSITE; PS50001; SH7.
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Mouse

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ABU04148
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5.1.6
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2005
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Aay72850 N
Aay72863 N
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Aay72866 N
Aay72860 N
Aay72861 N
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Aay67013 H
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Abc699714 H
Abc6995 H
Abc6995

Human Human Human Human Human

ALIGNMENTS

Location/Qualifiers
94. .110
//note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein" Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis; Mouse Stat3 protein fragment #14 (249-377 amino acids). Zhang X, Horvath C, Wrzeszcynska MH, Darnell JE, AAY72856 standard; protein; 129 AA: 99US-00387418. 30-AUG-2000; 2000WO-US023822 (first entry) (UYRQ) UNIV ROCKEFELLER WO200116605-A2 31-MAY-2001 Mus musculus 31-AUG-1999; 08-MAR-2001. AAY72856; therapy. Key Region AAY 7856

AAY 7866

AAY 78

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB

Length

Query

Score

Result Š.

WPI; 2001-226705/23.

Human pro Mouse Sta Mouse liv Mouse STA Human STA

N-termina Murine ST Human bai Mouse STA

Aay72855 Aay72854 Aay72854 Aay72854 Aae22055 Abb57164 Aae22056 Aar82995 Aar82995 Aay03768 Aay03768 Aay7289 Aab19964 Aar82999 Aab19964 Aae15174 Aae15996 Aar82999 Aab19964 Aar82999 Aae15174 Aae1599 Aae15994 Aae15174 Aae15994 Aae15994 Aae15994 Aae15994 Aae15994 Aae15994 Aae15994 Aae15174 Aay72861 Aay72

AAE22056 AAR82995 AAR82995 AAR82397 AAB12377 AAB12377 AAB14652 ABG69497 ABG69497 ABG69497

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AAY72856 AAY72855 AAY72854 AAY72841 AAE22055 ABB57164 AAE22054

Mouse 5

Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.

Claim 65; Page 80-81; 86pp; English.

Antipsori Human PRO Lung canc Rat Prote

Human pla Human sig Human Sta Human Pro Mouse Sta

ADD44738 AAR82993 AAB19964 AAE15174

AAB58442

ADD44740 AAY72861

The present sequence is mouse Stat3 protein fragment containing 249-377 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A

OM protein - pr	OM protein - protein search, using sw model
Run on:	May 25, 2005, 17:14:45 ; Search time 68.6634 Seconds (without alignments) 726.619 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-090-185-24 669 1 IACIGGPPNICLDRLENWITLNYQLKIKVCIDKDSGDVAA 129
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	2105692 segs, 386760381 residues
Total number of	Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 200000000
Post-processing	Post-processing: Minimum Match 00% Maximum Match 100% Listing first 45 summaries
Database :	A_Geneseq_16Dec04:* 1: _geneseq_1980s:* 2: _geneseq_1990s:* 3: _geneseq_200s:* 4: _geneseq_200s:* 5: _geneseq_200s:* 6: _geneseq_2003as:* 7: _geneseq_2003as:* 8: _geneseq_2003as:*

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Gaps

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Length 185; Indels

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The present sequence is mouse Stat3 protein fragment containing 155-377 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for tidentifying agents which modulates the interaction between a stat protein such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                    IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
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/note= "Stat3-c-Jun interaction region 2; corresponds to
342-358 position of Stat3 protein"
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                                                                                                                                                 57 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLBELQQKVSYKGDPIVQHRPMLEER
                                                                                                                      1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
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                                          Score 669; DB 4;
Pred. No. 6.8e-69;
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Best Local Similarity 100.
Matches 129; Conservative
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Sequence 185 AA;
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/note= "Stat3-c-Jun interaction region 2; corresponds to
342-358 position of Stat3 protein"
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  Stat protein comprises the N-terminal domain, coiled-coil domain, DNR binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                       100.0%; Score 669; DB 4;
100.0%; Pred. No. 4.2e-69;
iive 0; Mismatches 0;
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                                                                                                         Query Match
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                                                                   Sequence 129 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is mouse Stat3 protein fragment containing 107-377 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of typroliferative diseases and also for treating cancer and psoriaeis. A Stat protein comprises the N-terminal domain, colled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                     1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
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              Pred. No.
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100.0%; Pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
                                                                                                                        1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                       Human, signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypozia; stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; drave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion; Statbeta.
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100.0%; Score 669; DB 4;
100.0%; Pred. No. 1.1e-68;
iive 0; Mismatches 0;
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N-PSDB; AAD35066.
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              129; Conserv
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tissue ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, tranuma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, critogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus crythematosus, multiple sclerosis, insulin dependent diabetes mellitus, crychematosus, multiple sclerosis, insulin dependent diabetes mellitus, crychematosus, multiple sclerosis, insulin dependent diabetes mellitus, crychemia, autoimmune disease, primary biliary cirrhosis, pernicious mixed connective tissue disease, primary biliary cirrhosis, pernicious cracanicamune thyroiditis, idiopathic Addison's disease, vicuamatoid arthritis, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating cracinity, bullous pemphigoid, discoid lupus, ulcerative colitis and cardinomas e.g., bladder carcinoma, colon carcinoma, chomes earcomas and carcinoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human creating statibles are desposed to the present sequence is human creating cracinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 669; DB 5; Length 720; 100.0%; Pred. No. 4.2e-68; cive 0; Mismatches 0; Indels (
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Matches 129, Conservative
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N-PSDB; ABI99454.
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample comprising the expression profile of a gene group in the sample comprising selected from (1). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB19202 to AB19912), encoding the protein sequences in ABB5702 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression corprising produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by measuring
           Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or determining the expression profile of a gene group comprising these
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100.0%; Score 669; DB 5;
Best Local Similarity 100.0%; Pred. No. 4.6e-68;
Matches 129; Conservative 0; Mismatches 0;
                                                                                                                     Claim 2; Page 1084-1087; 2690pp; English
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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription of 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemia, condition or disorder which is the result of stroke, ischaemia, coronary atheroselerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, crissue ischaemia in the lower extremities, infarction, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, cpilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy critical meliorating a symptom of an autoimmune isease such as systemic lupus erythematosus, multiple sclerosis, insulin dependent diabetes mellitus, claminer syndrome, soleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, infarting vicinchosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, anaemia, autoimmune thyroiditis, disopathic Addison's disease, vitiligo, disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, and disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, and charca charcair disease when method is useful in preventing or treating and charca charcair disease when method is useful in preventing or treating
                                                                                                                                                                                                                                                                    Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human Stat3
                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 83-85; 94pp; English.
                                                                                                                                       Dalton W;
  08-SEP-2000; 2000US-0231212P
                                                                                                                                       Pardoll D, Jove R,
                                                  (UYSF-) UNIV JOHNS HOPKINS.
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100.0%; Score 669; DB 5;
100.0%; Pred. No. 4.6e-68;
iive 0; Mismatches 0;
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Matches 129; Conserv
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AAE22056 standard; protein; 769 AA.
                                             25-JUL-2002 (first entry)
                          AAE22056;
AAE22056
          SAXXEX
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RESULT 8

immune response; Stat3; coronary atterosclerosis; vascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; hypoxlycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; crave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion. transducer and activator of transcription 3; ischaemia Human protein related to angiogenesis regulation. Homo sapiens.

Dalton W; 10-SEP-2001; 2001WO-US028254. 08-SEP-2000; 2000US-0231212P. Yu H, Pardoll D, Jove R, (UYJO) UNIV JOHNS HOPKINS. (UXSF-) UNIV SOUTH FLORIDA. WPI; 2002-362218/39.

WO200220032-A1

14-MAR-2002.

Modulating anglogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator of transcription 3.

Disclosure; Page 83-85; 94pp; English.

coclusion, prenatal or postnatal oxygen deprivation, transma, vascular cocclusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus cryptematosus, multiple sclerosis, innulin dependent diabetes mellitus, Sjogram's syndrome, scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, dispathic thrombocytopenia purpura, Grave's disease, Goodpasture's dispathic thrombocytopenia purpura, Grave's disease, Goodpasture's dispathic thrombocytopenia purpura, Grave's disease, colitis and dense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, ilbrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, assemble method is also used in gene therapy. The poprotein related to angiogenesis regulation

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                                       100.0%; Score 669; DB 5; Length 769; 100.0%; Pred. No. 4.6e-68; ive 0; Mismatches 0; Indels (
                                         Query Match 100.
Best Local Similarity 100.
Matches 129; Conservative
Sequence 769 AA;
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Gaps

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249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIXKLEELQQKVSYKGDPIVQHRPMLEER
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                                                                                                                                                                                                                                                                     Signal transducer and activator of transcription; STAT; 19sf6; Stat3; receptor recognition factor; transcription factor; cellular debilitation; derangement; dysfunction; interferon-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.
                          1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                        IVELFRAIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI
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100.0%; Score 669; DB 2;
Best Local Similarity 100.0%; Pred. No. 4.6e-68;
Matches 129; Conservative 0; Mismatches 0;
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                                                                                                                                                                            AAR72082 standard; protein; 770 AA.
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93US-00126595.
94US-00212184.
94US-00212185.
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(first entry)
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N-PSDB; AAQ89340.
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11-MAR-1994;
11-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Darnell JE,
                                                                                                                                                                                                                      25-MAR-2003
27-SEP-1995
                                                                                                                                                                                                                                                      Mouse Stat3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a mouse acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (IL-6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA library using a polymerse chain reaction product (amplified using primers derived from an IL-6-treated mouse liver peptide) as a probe. APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or ribozymes, may be used to treat diseases induced by IL-6, e.g. inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
New acute phase response factor - for developing inhibitory agents for treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; acute phase response factor; transcription factor; interleukin-6; signal transmission; liver; antibody; antisense; ribozyme; antiinflammatory; antitumor; hypotensive; therapy.
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100.0%; Pred. No. 4.6e-68;
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Best Local Similarity 100..
...hes 129; Conservative
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369 DKDSGDVAA 377
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                                                                                                                                                                                                                                                                                          Homo sapiens
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AAB12377
ID AAB127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse signal transducer and activator of transcription (STAT) protein STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from ligand-activated receptor kinase complexes followed by nuclear translocation and DNA binding to activate transcription. Recombinant STAT4 can be obtd. using cDNA clone 198f6 (AAT31278) obtd. from splenic/thymic cells. STAT4 includes a DNA-binding domain (see also AAW03167) capable of both receptor recognition and message delivery via DNA binding in a receptor-ligand specific manner. STAT proteins and their DNA binding domains (see also AAW03165-75) are useful for screening antagonists used to inhibit STAT-mediated signal transduction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New STAT protein DNA-binding domain peptide(s) - useful for diagnosing, preventing or treating cellular dysfunction, e.g. oncogenesis, inflammation, parasitic disease or autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 IVELFRNIAKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLVKFPELNYQLKIKVCI
                                                                                                                                                                                                                      STAT; STAT4; signal transducer and activator of transcription; DNA binding protein; ligand; receptor; oncogenesis; inflammation; autoimmune disease; antagonist; therapy.
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100.0%; Pred. No. 4.6e-68;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                     398. .508
/label= DNA binding_domain
/note= "Claim 3, page 110"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 87-90; 138pp; English.
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                                                                                            AAW03176 standard; protein; 770 AA.
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Best Local Similarity 100.
Matches 129; Conservative
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DKDSGDVAA 377
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                                                                                                                                                             24-OCT-1996
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                                                                                                                                                                                          Mouse STAT4
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                369
                                                                                                                           AAW03176;
                                                                                                                                                                                                                                                                                                                        Key
Domain
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The present sequence represents a predominant allelic variant of human Signal Transducer and Activator of Transcription 3 (STAT3) protein, an intracellular transcription factor which mediates IL-6 signals. The encoding sequence differs from the original published human STAT3 gene sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3 protein is useful as a medicament or pharmaceutical composition for treatment of autoimmune or inflammatory diseases
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                                                                                                                                                                                                                                                           Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6; intracellular transcription factor; interleukin-6; medicament; variant; pharmaceutical; autoimmune disease; inflammatory; human.
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'AAY03768 standard; protein; 770 AA.
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                                                                                                                                                                                                 Human STAT3 allelic variant
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N-PSDB; AAX29281.
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The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater than S.O Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New crystals of an N-terminal fragment of a signal transducer and activator of transcription that effectively diffracts x-rays, useful for drug screening and development.
                                                                          STAT; signal transducer and activator of transcription; crystal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 669; DB 3; Length 770; 100.0%; Pred. No. 4.6e-68; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                      alpha helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuriyan J;
                                                   N-terminal domain of murine STAT-3 protein.
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/label= 3(10) helix of
28. .33
/label= Alpha helix 3
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43. .47
/label= Alpha helix 5
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/label= Alpha helix 1
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|abel= Alpha helix
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/label= Alpha helix
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                                                                                                                                                                                                                                                                                                                 50. .73
                                                                                        drug design; murine.
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                         08-NOV-2000
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AAB12377;
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The invention relates to methods for detecting compounds that bind to signal transducer and activator of transcription (STAT) proteins for the discovery and development of new drug compounds based on the structural properties of the protein crystal. The methods include: identifying a compound that binds to the N-terminal domain of a STAT protein, compound that binds to each other and/or their nucleic acid binding of the dimers to each other and/or their nucleic acid binding site; or identifying a compound that enhances or diminishes the ability of STAT protein dimers to induce the expression of a gene operably under the control of a promoter containing at least two adjacent weak binding sites for STAT protein dimers. The methods are used for identifying new drugs. An antagonist of STAT N-terminal dimeric interactions that control of a gene could be useful as drugs in the treatment of diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other contains the useful as drugs in the treatment of diseases e.g. anaemia, thrombocytopaenia, cancer, obesity, viral diseases and conturpaenia, thrombocytopaenia, cancer, obesity, viral diseases and content of a procession. The present sequence is murine STAT3 protein
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                                                                                                                                                                                                                                                                                                                                  Signal transducer and activator of transcription; STAT3; drug development; drug discovery; crystal; inflammation; allergy; asthma; leukaemia; anaemia; neutropaenia; thrombocytopaenia; cancer; obesity; viral disease; growth retardation; murine.
309 IVELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Conserved N-terminal domain of the STAT family"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying compounds that bind to signal transducer transcription proteins, useful for the production of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                          AAE14652 standard; protein; 770 AA.
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                                 249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLESLQQKVSYKGDPIVQHRPMLEER 308
                                                                                       61 IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
                                                                                                             Human, yeast two-hybrid assay, adipocyte, bait protein, NIDDM,
non-insulin diabetes mellitus, obesity, selected interacting domain, SID,
protein-protein interaction map, PIM, anorectic, metabolic disorder.
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             1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                    ABG69497 standard; protein; 770 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-DEC-2001; 2001WO-EP015423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JAN-2001; 2001US-0259377P.
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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(CNRS ) CENT NAT RECH SCI.
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The present sequence represents a member of the protein complex of the invention, used as the bait protein in the yeast two- hybrid assay
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Job time : 70.83 secs
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sequence 22, Appl
Sequence 19, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 12, Appl
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-387-418A-23
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                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence 24, Application US/09387418A

Patent No. 6391572
GENERAL INFORMATION:
APPLICANT: Shang, Xiaokui
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Darnell Jr., James B
ITILE OF INVENTION: NETHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
SOURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
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Patent No. 6391572
GENERAL INFORMATION:
GENERAL INFORMA
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APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENT IN VET. 2.0
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APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Zilong Shong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESSE: Alauber & Jackson
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 669; DB 3;
100.0%; Pred. No. 1.5e-68;
tive 0; Mismatches 0;
Wrzeszczynska, Melissa H
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; Patent No. 5716622
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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Best Local Similarity 100.
Matches 129; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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; ORGANISM: Mus musculus
US-09-387-418A-9
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STATE: New Jersey
COUNTRY: USA
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APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 669; DB 3; Length 185; Best Local Similarity 100.0%; Pred. No. 8.9e-69; Matches 129; Conservative 0; Mismatches 0; Indels
                   CURRENT APPLICATION NUMBER: US/09/387,418A CURRENT FILING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 43 SOFTWARE: Patentin Ver. 2.0
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Patent No. 6391572
BERRAL INFORMATION:
APPLICANT: Zhang, Xiaokui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 129; Conservative
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CORGANISM: Mus musculus
US-09-387-418A-22
                                                                                                                                                                        TYPE: PRT ORGANISM: Mus musculus
    FILE REFERENCE:
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US-09-387-418A-9
                                                                                                                                                  LENGTH: 185
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APPLICANT: Zilong Wen
APPLICANT: Zilong Wen
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Curt M. Horvath
APPLICANT: Chong Zhong Z
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309 IVELFRNLMKSAFVVFRQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 368
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100.0%; Score 669; DB 2; Length 7:
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
.APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08852091
Patent No. 5883228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 411 Hackengack Avenue
CITY: Hackengack
STATE: New Jersey
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TELEPHONE: 201 487-5800
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                    DKDSGDVAA 129
                                                                                                                                                                369 bkbscbvaa 377
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                                                                                                                                                                                              0; Indels
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APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Akira, Shizuo
TILLE OF INVENTION:
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEB: SUGHRUE, MION, ZINN, MACPEÀK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
                                                                                                                           100.0%; Score 669; DB 1
100.0%; Pred. No. 6e-68;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/08416581B Patent No. 5719042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 03.9:
REFERENCE/DOCKET NUMBER: 0-:
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (202)293-7060
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amino acid
                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 129, Conservative
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Best Local Similarity 100.
Matches 129; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                              MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 DKDSGDVAA 129
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TOPOLOGY: linear
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                                                               US-08-369-796-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 770 amino acids
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amino acid
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Best Local Similarity 100.
Matches 129; Conservative
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MOLECULE TYPE: protein
US-08-956-652-12
                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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                                        GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYEE: CIPOPDY disk
COMPUTER: IBM PC COMPATIBLE
OMBRATHOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
RIOR APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1997
APPLICATION NUMBER: US 07/980,498
FILING DATE: 19-MAR-1992
PRIOR APPLICATION NUMBER: US 07/980,498
FILING DATE: 19-MAR-1992
PRIOR APPLICATION NUMBER: US 08/2669
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/2669
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 19-MAR-1993
ATFORNEY AGENT INFORMATION:
TELEFAR INGORMATION NUMBER: 24-5800
TELEFAR INGORMATION NUMBER: 20-143-1684
TELECOMMUNICATION INFORMATION:
TELEFAR: 20-134-1684
TELEFAR: 133521
INFORMATION FOR ERQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
IPMCTH: 770 amino acids
Sequence 12, Application US/08820754 Patent No. 5976835
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amino acid
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Matches 129; Conservative
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249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308 61 IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120 1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 0; Gaps 100.0%; Score 669; DB 3; Length 770; 100.0%; Pred. No. 6e-68; ive 0; Mismatches 0; Indels (APPLICANT: Schindler, Christian W. APPLICANT: Schindler, Christian W. APPLICANT: Schindler, Christian W. APPLICANT: Schindler, Christian W. APPLICANT: Fu, Xian-Yuan APPLICANT: Wen, Zilong APPLICANT: Zhong, Zhong TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALauber & Jackson STREET: 411 Hackensack Avenue COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652 NAME: Jackson Egg., David A.
REGISTRATION NUMBER: 26,742
REPERRENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800 PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-MOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR PAPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: 13-MAR-1093 ; Sequence 12, Application US/08956552; Patent No. 6013475; GENERAL INFORMATION:

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249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
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100.0%; Score 669; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                        E: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                       APPLICANT: Vinkemeier, Uwe
APPLICANT: Moarefi, Ismail
APPLICANT: Darnell, Jr., James E.
APPLICANT: Lariyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-
TITLE OF INVENTION: STAT PROTEIN AND ME
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-491-5800
TELEFAX: 201-343-1684
                                                                                                                                                                         Sequence 8; Application US/09012710 Patent No. 6087478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
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                                             369 DKDSGDVAA 377
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HYPOTHETICAL:
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                                                                                                                                                     APPLICANT: Darnell Jr., James E.

APPLICANT: Schindler, Christian W.

APPLICANT: Schindler, Christian W.

APPLICANT: Wen, Zilong

APPLICANT: Zhong, Zhong

TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN

TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauher f.

STRPERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 669; DB 3; Length 770; 100.0%; Pred. No. 6e-68; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRICA APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackbon E8q., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/956,869
                                                                                                                                                  Sequence 12, Application US/08956869
Patent No. 6030808
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/212,185
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Hackensack Avenue CITY: Hackensack STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 770 amino acids
amino acid
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Best Local Similarity 100.0
Matches 129; Conservative
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                         369 DKDSGDVAA 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07601
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121
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Query Match 100.
Best Local Similarity 100.
Matches 129, Conservative
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                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                   SEQ ID NO 3
LENGTH: 770
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APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Pu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION PACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                             ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 669; DB 3
100.0%; Pred. No. 6e-68;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICANIUM:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
RELESARIA: 201 343-1684
FELEX: 133521
INFORMATION FOR SEG ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               770 amino acids
amino acid
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US-08-948-547-12
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RESULT 13

308 309 IVELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 368 Sequence 3, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USPENCIFFRATIVE CELLULAR CHANGES
TITLE OF INVENTION: DYSPROLIFFRATIVE CELLULAR CHANGES
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0 US-09-364-970-5

Sequence 5, Application US/09364970

Sequence 5, Application US/09364970

GENERAL INFORMATION:

APPLICANT: Bromberg, Jacqueline

TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR

TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING

TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES

TITLE OF INVENTION UNMBER: US/09/364,970

CURRENT PELLING DATE: 1999-07-31

NUMBER OF SEQ ID NOS: 10

SOSFWARE: PATENTIN Ver. 2.0 249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER Gaps ; 0 DB 3; Length 770; 100.0%; Score 669; DB 3; Length 770; 100.0%; Pred. No. 6e-68; Live 0; Mismatches 0; Indels (Query Match
100.0%; Score 669; DB 3; Length 7'
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 369 pkpsgpvAA 377

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249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 IVELFRNIAMKSAFVVERQPCMFWHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 368
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US-09-556-273-8
Sequence 8, Application US/09556273
Sequence 8. Application US/09556273
Sequence 8. Application
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
APPLICANT: Marafi, Ismail
APPLICANT: Darnell, Jr., James E.
APPLICANT: Rarlyan, John
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 770;
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                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 13
CORRESPONDENCES: 13
CORRESPONDENCES: 13
CORRESPONDENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: 411 Hackensack Avenue, 4th Floor
CITY: 411 Hackensack
STATE: 105
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
CORPTARE: 1BM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/556,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Bey, David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECHONE: 201-487-5600
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFCATION:
PRICE APPLICATION DATA:
APPLICATION NUMBER: 09/012,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 770 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 DKDSGDVAA 129
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369 DKDSGDVAA 377
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Search completed: May 25, 2005, 17:47:38 Job time : 17.141 secs

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Sequence 24, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-090-185-24
                                                                        May 25, 2005, 17:36:58 ; Search time 56.4935 Seconds (without alignments) 763.830 Million cell updates/sec
                                                                                                                                                          1 IACIGGPPNICLDRLENWIT.....LNYQLKIKVCIDKDSGDVAA 129
                                                                                                                                                                                                                                                                                                                                                                       1434725
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                             1434725 seqs, 334507595 residues
                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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669
                                                                                                                                              Perfect score:
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                                                                                                                                                            Sequence:
                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 24, Appl	Sequence 23, Appl	Sequence 22, Appl	Sequence 9, Appli	4	7	Sequence 5, Appli	Sequence 12, Appl	Sequence 8, Appli	Sequence 56, Appl	Sequence 2, Appli	Sequence 12, Appl	Sequence 780, App
ΩI	US-10-090-185-24	US-10-090-185-23	US-10-090-185-22	US-10-090-185-9	US-10-380-020-4	US-10-380-020-2	US-10-380-020-5	US-09-876-773-12	US-10-045-792-8	US-10-038-010-56	US-10-117-087-2	US-10-639-617-12	US-09-925-302-780
	13	13	13	13	15	15	15	11	14	14	14	11	6
* Query Match Length DB	129	185	223	271	720	769	769	770	770	770	770	770	793
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	699	699	699	699	699	699	699	699	699	699	699	699	699
Result No.	-	7	m	4	S	9	7	a 0	σ	10	11	12	13

Sequence 780, App Sequence 329, App Sequence 349, App Sequence 18, Appl Sequence 30, Appl Sequence 31, Appl Sequence 31, Appl Sequence 29, Appl		Sequence 5, Appli Sequence 2, Appli Sequence 1, Appli Sequence 44, Appli Sequence 44, Appl Sequence 823, App Sequence 19, Appl	39, A
10 US-09-925-302-780 15 US-10-116-275-329 13 US-10-090-185-18 13 US-10-090-185-18 13 US-10-090-185-30 13 US-10-090-185-31 13 US-10-090-185-31 13 US-10-090-185-31 13 US-10-090-185-31	13 US-10-090-185-25 13 US-10-090-185-15 13 US-10-090-185-15 14 US-10-090-185-12 14 US-10-245-120-3 11 US-09-876-773-6 14 US-10-245-120-2 17 US-10-245-120-2	17 US-10-936-390-5 9 US-09-833-205-2 11 US-09-876-773-4 14 US-10-245-120-1 14 US-10-308-279-44 16 US-10-755-889-352 16 US-10-755-889-351 17 US-10-492-043-19	17 US-10-639-617-4 9 US-09-935-297-550 9 US-09-833-205-4 9 US-09-813-205-6 11 US-09-876-773-8 14 US-10-045-792-7 14 US-10-205-194-39
2229 2229 2229 2229 2229	213 236 236 282 712 712	712 750 750 750 750 750	750 7486 7449 7499 749
100 999.6 999.6 85.4 85.4 44.68	65.2 65.2 65.2 65.2 65.2 65.2	65522222222222222222222222222222222222	65.2 64.6 64.6 64.6 65.0 65.0 65.0 65.0
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114 115 116 119 119 220 22	3.2.2.2.2.2.3.4 3.2.2.2.2.5.4.3.4	31 32 33 34 34 36 36	0 4 4 4 4 4 4 9 0 U U U U U U U U U U U U U U U U U U

ALIGNMENTS

APPLICANT: WIZESZZYJNKA, Melissa H APPLICANT: WIZESZZYJNKA, Melissa H APPLICANT: Horvath, Curt M APPLICANT: Horvath, Curt M APPLICANT: Barnell Jr., James E APPLICANT: Darnell Jr., James E APPLICANT: Darnell Jr., James E APPLICANTON: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR TITLE OF INVENTION: INTERACTIONS FILE REFERENCE: 600-12-53 CURRENT FILING DATE: 2002-03-04 PRIOR APPLICATION NUMBER: 09/387,418 PRIOR APPLICATION NUMBER: 09/387,418 PRIOR APPLICATION NUMBER: 09/387,418 SUFTWARE: PATENTIN Ver. 2.0 EQ ID NO 24 LENGTH: 129 TYPE: PATENTIN MUS musculus ORGANISM: Mus musculus	h Similarity 100.0%; Pred. No. 9.6e-67; 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 IACIGGPPNICLDRLENWITSLAESQLOTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 60	1 IVELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
APPLICANT: WIZEGEZCYBERA APPLICANT: HOTVAIL, CUIT APPLICANT: DATNELL CUIT TITLE OF INVENTION: METHO TITLE OF INVENTION: INTE FILE REPRENENCE: 600-1-253 CURRENT APPLICATION NUMBER: PRIOR PLING DATE: 209-0 PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMB	Query Match Best Local Similarity 100. Matches 129; Conservative		61
		8 8	8 8

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Sequence 4, Application US/10380020
; Sequence 4, Application US/10380020
; Publication No. US2004005276A1
; GENERAL INFORMATION:
    APPLICANT: Vu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Dalton, Willian
; TITLE OF INVENTION STAt3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT PILING DATE: 2003-03-07
; PRIOR PPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Version 3.0
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wzzeszzynska, Melissa H
APPLICANT: Horvath, Cutr M
APPLICANT: Horvath, Cutr M
APPLICANT: Horvath, Cutr M
APPLICANT: Horvath, NETHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFRENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
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                                                   95 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 154
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SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.
Matches 129; Conservative
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CRGANISM: Mus musculus
US-10-090-185-9
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Sequence 22, Application US/10090185

Sequence 22, Application US/10090185

Publication No. US20020197647A1

GENERAL INFORMATION:

APPLICANT: Zhang, Xiaokui

APPLICANT: Wreaczcynka, Melissa H

FITLE OF INVENTION: INTRACTIONS

FILE REFERENCE: 600-1-253

CURRENT FILING DATE: 2002-03-04

PRIOR PILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 22

LENGTH: 223
                                                                                                                                                      GENERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT Zhang, Xiaokui

APPLICANT Zhang, Xiaokui

APPLICANT Barnell Jr., Jamee B

TITLE OF INVENTION: INTERACTIONS

FILE REFERENCE: 600-11-253

CURRENT FILING DATE: 1999-08-31

PRIOR PELICATION NUMBER: 09/387,418

PRIOR PELICATION NUMBER: 09/387,418

PRIOR PELICATION NUMBER: 09/387,418

SOFTWARE: PATENTING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43
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100.0%; Pred. No. 1.9e-66;
Live 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.5e-66;
Matches 129; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 129; Conservative
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CAGANISM: Mus musculus
US-10-090-185-23
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249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
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Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                  Length 769;
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                                                                                                                                                                                                                                                                Query Match 100.0%; Score 669; DB 15; Best Local Similarity 100.0%; Pred. No. 9.6e-66; Matches 129; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Jackson Egg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 11.MAR-1994
APPLICATION NUMBER: US:07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-JUN-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
    CURRENT APPLICATION NUMBER: US/10/380,020 CURRENT FILING DATE: 2003-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09876773
Publication No. US20040058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
                        CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION WUMBER: 60/231,212
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
LENGTH: 769
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; ORGANISM: Homo Sapiens
US-10-380-020-5
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APPLICANT: Pardoll, Drew
APPLICANT: Datco, Richard
APPLICANT: Jove, Richard
APPLICANT: Journal Millian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-003-999
CURRENT APPLICATION NUMBER: 60/231,212
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
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APPLICANT: Pardoll, Drew
APPLICANT: Pove, Richard
APPLICANT: Jove, Millian
TITLE OF INVENTION, Willian
FILE REFERENCE: 10873-009-999
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8.8e-66;
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100.0%; Pred. No. 9.6e-66;
tive 0; Mismatches 0;
                                                                                                          Query Match
100.0%; Score 669; D
Best Local Similarity 100.0%; Pred. No. 8.8
Matches 129; Conservative 0; Mismatches
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Publication No. US20040052762A1
GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/10380020 Publication No. US20040052762A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 129; Conservative
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                                        , ORGANISM: Homo Sapiens
US-10-380-020-4
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LENGTH: 769
LENGTH: 720
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SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: STAT3 : Transcription factor
; LOCATION: (1)..(770)
; OTHER INFORMATION:
US-10-038-010-56
STRANDEDNESS: single
                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 129; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-10-038-010-56
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US-10-117-087-2
                                                                                                US-10-045-792-8
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                                                                                                                                                                                                                                                                                                      Gaps
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Publication No. US20030003563A1
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
Moarefi, Ismail
Darnell, Jr., James B.
Kuriyan, John A. Chystal OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                 Length 770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
                                                                                                                                                                                                                                                              Query Match
100.0%; Score 669; DB 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0;
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APPLICATION NUMBER: US/09/012,710
FILING DATE: -Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
                                                      TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-Oct-2001
CLASSIFICATION: <UNKNOWD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 770 amino acids TYPE: amino acid
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                    TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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INFORMATION FOR SEQ ID NO: 8:
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 56, Application US/10038010
PUDLICATION NO. US20030040089A1
GENERAL INFORMATION:
APPLICANT: PIETE LEGITAIN
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
TITLE OF INVENTION: PROTEIN PROTEIN ADMER: US/10/038,010
CURRENT APPLICATION NUMBER: US 60/259,377
FRICE RILING DATE: 2001-01-02
NUMBER: OF SEQ ID NOS: 67
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Query Match 100.0%; Score 669; DB 14; Length 770; Best Local Similarity 100.0%; Pred. No. 9.6e-66; Matches 129; Conservative 0; Mismatches 0; Indels 0
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61 IVELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
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                                                                                                                                                                                                                                                                                                                                Length 770;
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FILE REFERENCE: PAIO4
FILE REFERENCE: PAIO4
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
FRIOR FILING DATE: 2000-03-08
FRIOR FILING DATE: 2000-03-08
FRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 780
LENGTH: 793
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                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                              100.0%; Score 669; DB 17;
100.0%; Pred. No. 9.6e-66;
tive 0; Mismatches 0;
                                     : 600-1-073 CIP
                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
               REGISTRATION NUMBER: 26,742
                                     REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-925-302-780

; Sequence 780, Application US/09925302

; Patent No. US20020044941A1

; GENERAL INFORMATION:
                                                                                                                INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino scids
                                                                        TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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Best Local Similarity 100.
Matches 129; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    Similarity
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US-09-925-302-780
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                                                                                                                                                                                                                                                                                                          Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
TLING DATE: 12-Aug-2003
CLASSIFICATION 435
PRIOR APPLICATION 435
FILING DATE: 11-Aug-1094
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-Aug-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                  Indels
TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STATS
FILE REFERENCE: SERLUPI=2
CURRENT APPLICATION NUMBER: US/10/117,087
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US/09/526,542
PRIOR FILING DATE: 2000-03-19
WUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                      Score 669; DB 14;
Pred. No. 9.6e-66;
                                                                                                                                                                                                                                                                                                                                                Mismatches
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US-10-639-617-12

i Sequence 12, Application US/10639617

i Publication No. US20050079543A1

i GENERAL INFORMATION:

i APPLICANT: Darnell Jr., James E.

Fu. Xian-Yuan

Fu. Xian-Yuan

Wen, Zilong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                        100.0%;
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Best Local Similarity 100.
Matches 129; Conservative
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                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Human
US-10-117-087-2
                                                                                                                                                                         SEQ ID NO 2
LENGTH: 770
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121 DKDSGDVAA 129
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APPLICANT:
BIANGH, David
APPLICANT:
BIANGH, David
APPLICANT:
Lambkin, Imeda
APPLICANT:
Higgins, Lisa
APPLICANT:
Higgins, Lisa
APPLICANT:
Higgins, Lisa
APPLICANT:
FILE OF INVENTION:
Generic Analysis of Peyer's Patches and Methods and
TITLE OF INVENTION:
COMPOSITION:
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE:
SOFTWARE:
FILE REFERENCE:
FILE REPERENCE:
FILE REPERENC
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100.0%; Score 669; DB 10; Length 793;
Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 129; Conservative 0; Mismatches 0; Indels 0
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Pred. No. 2.1e-65;
1; Mismatches 0; Indels 0
Sequence 780, Application US/09925302;
Publication No. US20030064072A9;
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT FILING DATE: 2001.08-10;
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12;
NUMBER OF SEQ ID NOS: 896;
SOFTWARE: Patentin Ver. 2.0;
LENGTH: 793
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Publication No. US20030211476A1
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Best Local Similarity 99.2
Matches 128; Conservative
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CRGANISM: Homo sapiens
US-09-925-302-780
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; ORGANISM: Rat
US-10-116-275-329
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LENGTH: 770
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Search completed: May 25, 2005, 18:21:51 Job time : 59.8269 secs

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version	- 2005
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OM protein - protein search, using sw model

Run on:

25, 2005, 17:24:07; Search time 12.1698 Seconds (without alignments) 1019.898 Million cell updates/sec

US-10-090-185-24

699 Perfect score:

1 IACIGGPPNICLDRLENWIT......LNYQLKIKVCIDKDSGDVAA 129 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*

Database

pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ISGF3 p91-related	DNA-binding protei	interferon-depende	gamma-interferon a	interferon alpha-i	mammary gland fact	mammary gland fact		mammary gland fact	interleukin-4-indu	DNA-Binding Protei	microtubule bindin	hypothetical prote	type I site-specif	hypothetical prote			ovarian abundant m	probable transcrip	hypothetical prote	hypothetical prote		probable gtpase ac	60S RIBOSOMAL PROT	myosin-like protei	alpha-fetoprotein	hypothetical prote		
SUMMARIES	Ω	I49508	A54444	A46159	A56047	A46160	149274	S54772	G02317	855527	A54740	157557	H90279	T25063	NDECAS	B70042	F84840	T06667	A48461	B96003	T39082	G90550	G81420	T39954	T48076	T14277	A41948	F72253	AC2368	AF2374
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de	Query	100.0	99.3	58.4	56.1	38.4	24.0	24.0	24.0	21.2	14.6		12.0	12.0	11.8	11.7	11.7	11.7	11.5	11.3	11.3	11.2	11.2	11.2	11.1	11.1	11.1	11.1	10.9	10.9
	Score	699	664	390.5	375	257	160.5	160.5	160.5	142	86		80.5	80	79	78.5	78.5	78	77	75.5	75.5	75	75	75	74.5	74.5	74.5	74	73	73
	Result No.	-	7	m	4	ഹ	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT 2
A5444

Modebinding protein APRF - human
C;Species: Homo sapiens (man)
C;Date: 21-Peb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: A5444
R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sur

ribosomal protein	hypothetical prote	HST3 protein - yea	golgiñ-245 - moúse	xanthine dehydrode	hypothetical profe	protein T22C1.6 (i	4-hydroxyphenylpyr	4-hydroxyphenylpyr	myosin heavy chain	heat shock protein	conserved hypothet	hypothetical prote	probable protein k	unconventional myo	breast cancer susc
T00423	A85040	S54631	T14265	XORTDH	T25110	F87844	S32458	S32821	S21801	873360	A99345	A86253	F96558	A59310	T42205
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257	432	447	1218	1331	335	346	393	393	1999	217	328	573	879	1529	3329
10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.7	10.7	10.7	10.7	10.7	10.7
72.5	72.5	72.5	72.5	72.5	72	72	72	72	72	71.5	71.5	71.5	71.5	71.5	71.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C;Species: Mis musculus (house mouse)
C;Species: Mis musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149509; 149009
R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRP, a novel IFN-stimulated gene factor 3 p91-related tr A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: 149508
A;Accession: I49508
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-770 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P42227; GB:L29278; NID:G476715; PIDN:AAA37254.1; PID:g47671
R;Raz, R.; Durbin, J.E.; Levy, D.E.
Biol. Chem. 269, 24391-24395, 1994
A;Title: Acute phase response factor and additional members of the interferon-stimulate
A;Reference number: 149009; MUID:95014185; PMID:7523373
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C;Superfamily: human signal transducer and transcription activator STAT5A
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100.0%; Score 669; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.8e-55;
Matches 129; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: 149009
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
p91-related transcription factor - mouse
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A; Molecule type: DNA
A; Residues: 1-851 < YAN>
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Affitle: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa ISG A; Reference number: A46159; MUID:92366557; PMID:1502203
A; Accession: A46159
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Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related
A;Reference number: A54444; MUID:94208062; PMID:7512451
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                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Cross-references: UNIPROT:P40763; GB:L29277; NID:g475788; PID:g475789
C;Genetics:
A;Gene: GDB:STAT3; APRF
A;Cross-references: GDB:358950
A;Map position: 17q21-17q21
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                         Gabs
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C;Superfamily: human signal transducer and transcription activator STAT5A
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                                                                                                                                                                                                                                                                                                                                             Score 664; DB 2;
Pred. No. 5.5e-55;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; not compared wit
A;Molecule type: nucleic acid; protein
A;Residues: 1-739 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT: P42224
                                                                                                                                                                                                                                                                                                                                               99.3%;
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Matches 128, Conservative
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gamma-interferon activation site-binding protein Stat4 - mouse C;Species: Mus musculus (house mouse) C;Species: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

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A,Molecule type: mRNA
A;Residues: 1-748 <YAM>
A;Cross-references: UNIPROT:P42228; GB:U09351; NID:g509502; PIDN:AAA19692.1; PID:g50950
C;Superfamily: human signal transducer and transcription activator STATSA
C;Reywords: DNA binding; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NyAlternate names: stat2 protein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 2.1-Sep-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46160; S71908; S53873
R;Fu, X.Y.; Schindler, C.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator A;Reference number: A46160; MuID:92366558; PMID:1502204
A;Accession: A46160;
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R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.B.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in A;Reference number: S53873; MUID:95192056; PMID:7885841
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                                        B.L.; Gilbert, D.J.; Jenkins,
C;Accession: A56047
R;Yamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins Mol. Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Status: preliminary; nucleic acid sequence not shown
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A;Residues: 1-851 <FU1.
A;Cross-references: UNIPROT: P52630
A;Note: sequence extracted from NCBI backbone (NCBIP:110820)
B;Yan, R; Qureshi, S,; Zhong, Z;; Wen, Z;; Darnell, J.E.
submitted to the EMBL Data Library, December 1994
A;Reference number: S71908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.1%; Score 375; DB 2;
59.3%; Pred. No. 1.3e-27;
iive 19; Mismatches 31;
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A;Residues: 1-196;392-591;684-730 <YAW>
A;Cross-references: EMBL:U18671
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Matches 73; Conservative
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Matches 5
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A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:248538; NID:g758633; PIDN:CAA8 R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L. Proc. Natl. Acad. Sci. U.S.A. 92; 8831-8835, 1995 A; Hitle: Cloning and expression of Stats and an additional homologue (Stat5b) involved A;Reference number: 149273; MUID:96004632; PMID:7568026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:g1151169; PIDN:AAB06589.1; PID:g11
C;Superfamily: human signal transducer and transcription activator STATSA
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C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: $5527; $44353
EMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cyt
A;Reference number: $55527; MUID:95180809; PMID:7882907
A;Accession: $55527
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: Stat5a
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 24.0%; Score 160.5; DB 2; Length 793;
1 Similarity 37.6%; Pred. No. 3e-07;
38; Conservative 17; Mismatches 37; Indels 9
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A;Reference number: S54772; MUID:95237198; PMID:7720707
A;Accession: S54772
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-793 <MUI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.0%; Score 160.5; DB 2; 37.6%; Pred. No. 3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                    A;Accession: 149273
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-793 <RES>
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MyAlternate names: stats protein
MyAlternate names: stats protein
MyAlternate names: stats protein
C;Species us musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54772; 149273
R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
BMBO J. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:P42222; UNIPROT:O9JKM1; EMBL:U21110; NID:g747973; PIDN:AAC52 R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A. BEBD J. 1175, 1995
A,Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin-A,Reference number: S54772; MUID:95237198; PMID:7720707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-432, E',434-786 <MUI>
A;Cross-references: EMBL:Z48539; NID:g758635; PIDN:CAA88420.1; PID:g758636
R;Azam, W.; Erdjument-Baromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris, EMBO J. 14, 1402-1411, 1995
A;Title: Interleukin-3 signals through multiple isoforms of Stat5.
A;Reference number: S54725; MUID:95246733; PMID:7537213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NiAlternate names: STATS protein homolog p80
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149214; S54773; S54727
R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Rytile: Cloning and expression of Stats and an additional homologue (Statsb) involved
A;Reference number: 149273; MUID:96004632; PMID:7568026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                           121
                                                                                                                                                         305 TELLQRLLHRAFVVETQPCMPQTPHRPLILKTGSKFTVRTRLLVRLQEGNESLTVFEVSID 364
                                    265 GGPPEGSLDVLQSWCEKLAEIIWONROOIRRAEHLCOOLPIPG-PVEEMLAEVNATITDI 323
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         61
      ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                        62 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCID
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A;Status: preliminary
A;Status: preliminary
A;Residues: 1-432,'E',434-786 <AZA>
A;Residues: 1-432,'E',434-786 <AZA>
A;Genet: Statsb
C;Superfamily: human signal transducer and transcription activator STATSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 ISALVTSTFIIEKOP-----POVLKTOTKFAATVRLLV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: I49274
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-786 <RES>
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les 38; Conserv
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RN 366
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                                                                                                                                                                                                                                             122 KD 123
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A; Status: prelimina
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Best Local S
Matches 38
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A;Cross-references: UNIPROT:Q22633; EMBL:Z50016; PIDN:CAA90315.1; GSPDB:GN00021; CESP:T!
A;Experimental source: clone T21C12
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Jul-2004
C;Accession: T25063
                              A;Gene: STAT6
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R'Wilkinson, J.
submitted to, the EMBL Data Library, July 1995
A;Reference number: Z19976
A;Accession: T25063
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393 <WIL>
C;Genetics:
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                A;Cross-references: UNIPROT:P42231; EMBL:X78428; NID:g602354; PIDN:CAA55191.1; PID:g6023 A;Note: this is a revision to the sequence from reference S44353 R;Wakao, H.; Gouilleux, F.; Groner, B. EMBO J. 13, 2182-2191, 1994 A;Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcriple A;Reference number: S44353; MUID:94244619; PMID:7514531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Hou, J.; Schindler, U.; Henzel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 ICLDRLENW-------ITSLAESQLQTRQQIKKLEELQQKVSYKGDPI-VQHRP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 PPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Homo sapiens (man)
                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-716, 'RHLHGPGSLPSR',729,'P',731,'ASL' <WAW>
A; Cross-references: EMBL:X78428
A; Note: this sequence has been revised in reference S55527
C; Superfamily: human signal transducer and transcription activator STATSA
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A;Molecule type: mRNA
A;Residues: 1-848 <HOU>
A;Cross-references: UNIPROT:P42226
C;Superfamily: human signal transducer and transcription activator STATSA
C;Keywords: DNA binding; transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 265, 1701-1706, 1994
Affille: An interleukin-4-induced transcription factor: IL-4 stat. A;Reference number: A54740; MUID:94367369; PMID:8085155
A;Accession: A54740
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 21.2%; Score 142; DB 2; Length 794; Best Local Similarity 36.4%; Pred. No. 1.7e-05; Matches 36; Conservative 17; Mismatches 36; Indels
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A;Introns: 137/3; 236/3 A; Gene: CESP:T21C12.2

A; Map position:

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-837 <RES> A;Cross-references: UNIPROT:P52633; GB:L47650; NID:g1008876; PIDN:AAA79006.1; PID:g10088

A; Accession: 157557

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microtubule binding protein, probable [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 2-4-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H90279
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9UXN4; GB:AE006641; NID:g13814451; PIDN:AAK41495.1; GSPDB:C;Genetics:
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                                                                                                                         5 GGPPNICLDRLENWITSLAESQLQTRQQIXKLE-ELQQKVSYKGDPIVQHRPMLEERIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 RLENWITSLAESQLQTRQQIKKLEELQQKV--SYKG--DPIVQHRPML
                                                                                                                                                                                                                                           64 LFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVQFTTKVRLLV 105
                                                                                                                                                                                                                                                                                 264 VLRTLVTSSFLVEKQP------PQVLKTQTKFQAGVRFLL 297
ch 14.0%; Score 93.5; DB 2; Similarity 32.4%; Pred. No. 0.71; 33; Conservative 12; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 LNYQLKIKVCIDKDSGDVAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 V-YLIEIKSYVEKDDVNWAA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A99139
      Query Match
Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-464 <KUR>
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R;Cowan, G;M.; Gann, A.A.F.; Murray, N.E.
R=15 S6, 103-109, 1989
A;Title: Conservation of complex DNA recognition domains between families of restriction A;Reference number: A;32343; MUD:89089749; PMID:2642743
A;Accession: A;32343
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A, Residues: 1-589 <COW>
C; Comment: This S chain, one of three components (S, R, and M chains) of type I site-spe C; Comment: This S chain, one of three components (G, R, and M chains) of type I site-specificates the target sequence, GAG
C; Superfamily: type I site-specific deoxyribonuclease EcoA chain S
C; Keywords: DNA binding; hydrolase; restriction modification system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cipencies acillus subtile Subtiles Subt
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N/Alternate names: deoxyribonuclease, EcoA, S chain (ATP- and S-adenosyl-L-methionine-de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 ATSDKKAISQIQEYVDYYGGSGVQHIALNTSDIITALEALRARGCEFLSIPSSYYDNLKE 302
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C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 30-Jun-1993
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                                                                                                                                                                                 ; Pred. No. 5.5;
23; Mismatches 56; Indels
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                                                                                                                              DB 2;
C;Superfamily: 4-hydroxyphenylpyruvate_dioxygenase
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Best Local Similarity 24.4%; Pred. No. 11;
Matches . 31; Conservative 25; Mismatches
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                                                                                                                              Score 80;
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Best Local Similarity 20.8*
Matches 35; Conservative
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116 INPKIDV 122
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T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A.; Arseference number: A69580; MUID:98044033; PMID:9384377
A.; Accession: B70042
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF2275661 AAF73401.1; -.

R RSSP; PR2227; 1BGJ.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0006371; F:stagnal transducer activity; IEA.

R GO; GO:0003700; F:transcription factor activity; IEA.

R GO; GO:0007165; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:0007165; P:stagnal transduction; IEA.

R InterPro; IPR001217; STAT.

InterPro; IPR001217; STAT.

R Pfam; PF02164; STAT_alpha; 1.

R Pfam; PF02164; STAT_bind; 1.

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Cercopithecinae; Macaca.
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DD Q9N145

PRELIMINARY; PRT; 163 AA.

C Q9N145

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Signal transducer and activator of transcription (Fragment).
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100.0%; Score 669; DB 2; Length 1
Best Local Similarity 100.0%; Pred. No. 7.6e-55;
Matches 129; Conservative 0; Mismatches 0; Indels
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2774 HUMAN
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(without alignments)
1230.701 Million cell updates/sec
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P40763
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                               1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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STA3_BOVIN
STA3_HOVIN
STA3_MOUSE
STA3_RAT
Q6DV79
Q9PVX8
Q7ZXX3
Q7ZXX3
Q7ZXX3
Q6NV46
Q6NV46
Q6NV6
Q6NV76
Q6NV76
Q6NV76
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Q6NV76
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Q68D00
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
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Q6P6Q7
Q9QXK0
Q764M5
Q8C497
Q99K94
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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669
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Match Length DB
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Maximum DB
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                      Mammalia; Euther
NCBI_TaxID=9606;
           CCCCCETTT AREA TO THE TOTAL TOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SH2.
Phosphotyrosine (by JAK) (By similarity).
Phosphoserine (By similarity).
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Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STA3 HUMAN STANDARD, PRT, 770 AA.
P40763; O14916; Q9BW54;
01-F8B-1995 (Rel. 31, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  727 727 Phosphoserine (By similar: 770 AA; 87974 MW; 9CEB147C73E83274 CRC64;
05-JUL-2004 (Rel. 44, Created)
5-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
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Homo sapiens (Human).
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DOMAIN 580 670
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                                                                                                                                                Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
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                                                                                                                                                                                                                                  Bovinae; Bos
                                                                                                                  Name=STAT3;
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TISSUBERCE FROM N.A. (ISOFORMS 1 AND DEL-701).

TISSUB-Kidney, and Pancraas;

MEDLINE=22388257; bubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; bubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Idschul S.F., Zeeberg B. Buetow K.H., Schamen C.M., Schuler G.D.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Drownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rapak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Shevchenko Y., Boulfard G.G.,

Rhiching M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rederration and initial analysis of more than 15,000 full-length human
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PubMed=11773079; DOI=10.1074/jbc.M111486200;

Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;

Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;

Functional interaction of STAT3 transcription factor with the coactivator NcoA/SRCla.";

J. Biol. Chem. 277:8004-8011(2002).

-! FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6) responsive elements identified in the promoters of various acute-phase protein genes.
                                                                                                                                                  Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T., Yoshida Y., Sudo T., Naruto M., Kishimoto T., Mel S., Sudo T., Naruto G., Kishimoto T., Mel S., Sudo T., Naruto G., Reinalde Gattor 3 pg1-related transcription factor involved in the gp130-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE-95215843; PubMed=7701321;
Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
"Requirement of serine phosphorylation for formation of STAT-promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O. Rajkumar N., Yi Q., Nickerson D.A.;
Rajkumar N., Yi Q., Nickerson D.A.;
"SeattleSNPs. NHIBH HL6662 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                      TISSUE=Placenta; MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O., "Highly conserved amino-acid sequence between murine STAT3 and a revised human STAT3 sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 564-704 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION ON SERINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 213:119-124(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 77:63-71(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complexes."
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NCBI_TaxID=10090;
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P42227;
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    CONFLICT
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M GO; GO: 0005537; C: cytopplasm; TAS.

R GO; GO: 0005537; C: cytopplasm; TAS.

R GO; GO: 0005634; C: nucleus; TAS.

R GO; GO: 0005634; C: nucleus; TAS.

R GO; GO: 0005628; P: transcription factor activity; TAS.

R GO; GO: 000528; P: transcription factor activity; TAS.

R GO; GO: 0000122; P: negative regulation of transcription from P. .; TAS.

R GO; GO: 0000122; P: negative regulation of transcription from P. .; TAS.

R GO; GO: 0000125; P: negative regulation of transcription from P. .; TAS.

R GO; GO: 0000155; P: signal transduction; TAS.

R GO; GO: 0000115; P: 11.

R GO; GO: 0000117; STAT.

InterPro; IPR000980; STAT.

InterPro; IPR001017; STAT.

R Fam; PP02864; STAT_bind; 1.

R Fam; PP02865; STAT_bind; 1.

R Fam; PP02865; STAT_bind; 1.

R R M: PP02865; STAT_bind; 1.

R R M: R PS051TE; PS50001; SH2; 1.

R R Activator; Alternative splicing; DNA-binding; Nuclear protein; Canalarian; Pranscription regulation.
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
-!- PATHWAY: Involved in the gp130-mediated signaling pathway.
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOA1.
-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                  ISOId=P40763-2; Sequence=VSP_010474;
-!- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas.
-!- FTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, LIP, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity.
-!- SIMILARITY: Belongs to the transcription factor STAT family.
-!- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphotyrosine (by JAK) (By similarity).
Phosphoserine (By similarity).
Missing (in isoform Del-701).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VSP_010474.
Q -> K (in dbSNP:1803125)
                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VAR 018679.

Q -> H (in Ref. 1).

P -> S (in Ref. 1).

K -> N (in Ref. 1).

F -> Y (in Ref. 1).

V -> L (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTId=VAR_018683
                                                                                                            IsoId=P40763-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                EMBL, L29277; AAA58374.1; -.
EMBL, AJ012463; CAA10032.1; -.
EMBL, AY572796; AAS66986.1; -.
EMBL, BC006627; AAH00627.1; -.
EMBL; BC014482; AAH1482.1; -.
EMBL; AF029311; AAB84254.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFAC; T01493; -.
Genew; HGNC:11364; STAT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H-InvDB; HIX0013840; -.
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727
701
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460
548
561
667
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HSSP; P42227; 1BG1.
                                                                                                                         Name=Del-701;
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MOD_RES
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"Acute phase response factor and additional members of the interferon-
stimulated gene factor 3 family integrate diverse signals from
cytokines, interferons, and growth factors.";
J. Biol. Chem. 269:24391-24395(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c; TISSUB=Liver;
MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
Yoshida K., Sudo T., Maruto M., Kishimoto T.;
"Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
related transcription factor involved in the gp130-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhong Z., Wen Z., Darnell J.E. Jr.; "Stat2; a STAT family member activated by tyrosine phosphorylation in response to epideran growth factor and interleukin-6."; Science 264:95-98(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM STAT3B).
STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
MEDLINE=96016116; PubMed=7568080;
Schaefer T.S., Sanders L.K., Nathans D.;
"Cooperative transcriptional activity of Jun and Stat3 beta, a short form of Stat3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           response factor).
Name-Stat3; Synonyms-Aprf;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last amoutation update)
Signal transducer and activator of transcription 3 (Acute-phase
                                                                                          100.0%; Score 669; DB 1; Length 770; 100.0%; Pred. No. 4.6e-54; ive 0; Mismatches 0; Indels 0
   T -> A (in Ref. 1).
6C00632211C8012D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995)
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SEQUENCE FROM N.A. (ISOFORM STAT3A)
STRAIN=129/SvJ;
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730 730 T
770 AA; 88067 MW;
                                                                                      Query Match
Best Local Similarity 100.
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 DKDSGDVAA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathway.";
Cell 77:63-71(1994).
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SEQUENCE FROM N.A. (ISOPORM STAT3A).

STRAIN=FVBAN; TISSUE=Nammary gland;

MEDLINE=2238825; PubMed=1247932; October 10.1073/pnas.242603899;

MEDLINE=2238825; PubMed=12477932; October 10.1073/pnas.242603899;

MISCAINI S.F., Zebeberg B.L., Grouse L.H., Derge J.G.,

Altschul S.F., Zebeberg B., Buetow K.H., Schnefer C.F., Bhart N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garriaca A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Menner D.M., Madan A., Schehn J.B., Once than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (II-6) responsive elements identified in the promoters of various acute-phase protein genes. STAT3B interacts with the N-terminal part of UNI to activate such promoters in a cooperative way. PATHWAY: Involved in the gp130-mediated signaling pathway. SUBBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOAl (By similarity). SUBCELLUAR LOCATION: Cyroplasmic; translocated into the nucleus in response to phosphorylation.

ALTERNATIVE PRODUCTS:

SVent_ALLernative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9; Wen Z., Zhong Z., Darnell J.E. Jr.; Maximal activation of transcription by Stat1 and Stat3 requires both tyrosine and serine phosphorylation."; Cell 82:241-250(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISOId=P4227-3; Sequence=VSP 010475;
TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and
kidney. STAT3B is also detected in the liver, although in a much
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 394:145-151(1998).
PubMed=11161808; DOI=10.1006/geno.2000.6433; Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T., Bewar K., Hennighausen L.; Structure of the mouse stat 3/5 locus: evolution from Drosophila zebrafish to mouse.
                                                                                                                                                                                   STRAIN=C57BL/6J, and NOD/LtJ;
Davoodi-Semiromi A., She J.-X.;
"A mutant Stat5b with weaker DNA binding defines a key defective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
MEDLINES-9931-9773; PubMed=9671298; DOI=10.1038/28101;
Becker S., Groner B., Mueller C.W.;
"Three-dimensional structure of the Stat3beta homodimer bound to
                                                                                                                                                                                                                                                     pathway in non-obese diabetic (NOD) mice.", Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P42227-2; Sequence=VSP_006287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P42227-1; Sequence=Displayed;
                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM STAT3A).
                                                                                                                   Genomics 71:150-155(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          less abundant manner.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Stat3A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphoserine.
TTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
FDMDLTSECATSPM -> FIDAVWK (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphotyrosine (by JAK) (By similarity).
          homodimers and maximal transcriptional activity (By similarity). SIMILARITY: Belongs to the transcription factor STAT family. SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                          EMBL; 129278; AAA19452.1; ---

EMBL; 106922; AAA19452.1; ---

EMBL; 106922; AAA19452.1; ---

EMBL; 106922; AAA19452.1; ---

EMBL; 108709; AAAC5668.1; ---

EMBL; AY29489; AAAC5418.1; ---

EMBL; AY29489; AAAC5418.1; ---

EMBL; AY29489; AAAC5418.1; ---

EMBL; AY29489; AAAC7418.1; ---

EMBC; ACC10005357; Erranscriptional activator activity; IDA.

GO; GO:0005159; Firtanscriptional activator activity; IDA.

GO; GO:0005515; Firtanscriptional activator activity; IDA.

GO; GO:0005515; Firtanscriptional activator activity; IDA.

GO; GO:0005515; Firtanscription from Pol II pro. ..;

EMBL; EMBC; EMBL; EMBL; EMBC; EMB
is important for the formation of stable DNA-binding STAT3
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/FIId=VSP 010475.
S-A: Decreased transcriptional
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S -> T (in Ref. 2 and 4).
M -> I (in Ref. 1).
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/FTId=VSP 006287
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noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                   249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
                                                                                                                                               309 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 368
                                                                                                                                 61 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IACIGGPPNICLDRLENWITSLASSQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 270:29998-30006(1995).
-!- FUNCTION: Transcription factor that binds to the interleukin-6
(IL-6)-responsive elements identified in the promoters of various
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998;
                                           Length 770;
                                                                 0; Indels
                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
Name-Stat3;
                                           100.0%; Score 669; DB 1;
100.0%; Pred. No. 4.6e-54;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                         770 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
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InterPro; IPR008967; P53_like_DNA_bnd.
InterPro; IPR000980; SH2.
                                                                                                                                                                                                                                                          PRT;
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                                                      Best Local Similarity 100.0
Matches 129; Conservative
                                                                                                                                                                                                                                                         STANDARD;
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InterPro; IPR001217; STAT

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                                                                                                                                                                                                                               similarity)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                               SMART, SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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GO; GO: 0004634; C:nucleus; IEA.
GO; GO: 0004770; F: signal transducer activity; IEA.
GO; GO: 0007242; P: intracellular signaling cascade; IEA.
GO; GO: 0006355; P: regulation of transcription, DNA-dependent; InterPro; IPR0008967; PS3 like_DNA_bnd.
InterPro; IPR0009967; SH2.
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                                                                                                                                                                                                                                                                                                                            Length 770;
                                                                                                                                                                                                                          Phosphotyrosine (by JAK) (By Phosphoserine (By similarity) D74A0C76954754ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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8.7e-54;
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727 727 P)
770 AA; 88039 MW;
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
SMART; SM00252; SH2; 1.
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Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
                                                                                                                                                                                                                                                                                                                                                   99.2%;
                                                                                                                                                                            Transcription regulation.
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Kenopus laevis (African clawed frog)
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    309 IVELFRNIMKSAFVVERQPCMPMHPDRPLVFKTGVQFTTKVRLLVKFPELNYQLKIKVCI 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005634; C:nucleus; IEA.
GO; GO:0006481; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000742; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008967; PSI.
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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                                                                                                                                                                                                                                                                                     Last annotation update)
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                                                                                                                                                                                                   769 AA
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Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                             Created)
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Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT_int; 1.
PROSITE; SM02525; SH2; 1.
PROSITE; PS550001; SH2; 1.
SEQUENCE 769 AA; 87974 MW;
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EMBL; AB017701; BAA86061.1; -.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RIA Klausner R.D., Collins F.S., Wagner L., Shemmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B. Buetcw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Editechenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robax S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,
RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Rhesley R.W., Toung A.C., Shevchenko Y., Bouffard G.G.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Scheutz J., Myers R.M., Butterfield Y.S.,
Rzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIRKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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97.2%; Score 650; DB 2; Length 76
Best Local Similarity 96.9%; Pred. No. 2.7e-52;
Matches 125; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC044717; AAH44717.1; -.
HSSP; P42227; 1861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87599 MW; 31018A3321CCEB9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR008967; P53 like_DNA_bnd.
InterPro; IPR008967; P53 like_DNA_bnd.
InterPro; IPR001217; STAT.
Pfam; PF00017; STAT alpha; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT_bind; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00252; SH
PROSITE; PS50001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                             NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 initiative.";
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Q7ZXK3 PRELIMINARY; PRT; 766 AA. Q7ZXK3; Q1-ZXK3; Q1-JUN-2003 (TrEWBLrel. 24, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) Stat3-A protein.

GERARA

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310 IVDLFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 369
                                                                                                                                               Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                 786 AA
                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00017; SHZ; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 121; Conservative
                                                                                 PRELIMINARY;
                              ||:||||||
|DKESGDVAA 378
                   121 DKDSGDVAA 129
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                                                                                                                             Stat3 protein.
                                                                                                  05-JUL-2004
05-JUL-2004
                                                                                                                                       Name=stat3;
                                   370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IACIGGPPNICLDRLETWITSLAESQLQIRQQIRKLEELQQKVSYKGDPIIQHRPALEEK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                           Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008967; PS3 like DNA bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.2%; Score 637; DB 2; Length 414; 93.8%; Pred. No. 2.2e-51; Live 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO45275; AAH45276.1; --
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STAT_int; 1.
AA; 48253 MW; OFPD1BS09B7526BD CRC64;
                                                                                        01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                               414 AA.
                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZDB-GENE-980526-68; stat3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
                                                                             1-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity ... Matches 121; Conservative
                                                              PRELIMINARY;
         |||||: ||
369 DKDSGEGAA 377
DKDSGDVAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 AA;
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                                                                                                                                                        Danio.
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                     Cyprinidae; Dani
NCBI_TaxID=7955;
                                                                                                          Stat3 protein.
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                                                                                                                     Name=stat3;
121
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RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altachus R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rabask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachy J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Annishki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Annishki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
R. Generation and initial analysis of more than 15,000 full-length human
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A Strausberg R.;

Rebell R.;

Rebell R.;

STIN; ZDB-GENE-980526-68; stat3.

Red; GO:0004534; C:nucleus; IEA.

Red; GO:0004371; F:signal transcription factor activity; IEA.

Red; GO:0007242; P:intracellular signaling cascade; IEA.

Red; GO:0006242; P:intracellular signaling cascade; IEA.

Red; GO:0006370; F:ranscription of transcription, DNA-dependent; IEA.

Red; GO:0006370; F:ranscription furanscription, DNA-dependent; IEA.

Red; GO:0006370; F:ranscription furanscription, DNA-dependent; IEA.

Red; GO:0006370; F:ranscription, DNA-dependent; IEA.

Red; GO:0006370; F:ranscription, DNA-dependent; IEA.

Red; GO:0006370; F:ranscription, DNA-dependent; IEA.
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                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90039 MW; FC7371D0B0E5447E CRC64;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
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250 IACIGGPPNICLDRLETWITSLAESQLQIRQQIRKLEELQQKVSYKGDPIIQHRPALEEK 309
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Actinopterygil; Neopterygil; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Signal transducer and activation of transcription factor 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                550001; SH2; 1.
806 AA; 92151 MW; 74BC4EA401C3C942 CRC64;
                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Danio rerio).
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                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                     370 DKESGDVAA 378
                                                                                                     DKDSGDVAA 129
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                                                                                                                                                                                                                                                                                                             Transcription factor.
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PROSITE; PS50001; SH
SEQUENCE 806 AA;
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093599
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Q6DVF3
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310 IVDLFRNIAMKSAFVVERQPCMPMHPDRPLVIKTGVQFTNKVRLLVKFPELNYQLKIKVCI 369
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                                                                                                                                                                                                                                                                                                       R BMBL; AX639947; AAT64912.1; -.
R GO; GO:0005634; C:nucleus; IEA.
R GO; GO:000471; F:ranscription factor activity; IEA.
R GO; GO:000471; F:ranscription factor activity; IEA.
R GO; GO:0007242; P:intracellular signaling cascade; IEA.
R GO; GO:0007242; P:intracellular signaling cascade; IEA.
R GO; GO:0007242; P:intracellular signaling cascade; IEA.
R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
R InterPro; IPR009967; P53_like_DNA_bnd.
R InterPro; IPR0017; STAT.
R Pfam; PF01017; STAT alpha; 1.
R Pfam; PF01017; STAT alpha; 1.
R Pfam; PF02865; STAT int; 1.
R PROSITE; PS50001; SEZ; Int; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVELFRNIMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLVKFPELNYQLKIKVCI
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05-JUL-2004 (TrEWBLrel. 27, Last sequence update)
05-JUL-2004 (TrEWBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Signal transducer and activator of transcription 3 isoform 1.
Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Nerteleostei; Neoteleostei; Beloniformes; Adrianichthyidae; Oryziinae; Oryziae.
                                                         Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
BMBL, AX64134, AAT46364.1;
GO; GO:0006534; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:000740; P:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:000555; P:regulation of transcription, DNA-dependent; IEA.
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                       Liu R., Hong Y.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
Oryzias latipes (Medaka fish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 93.8
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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DKESGDVAA 378
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767 AA

PRT;

PRELIMINARY;

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                                                                                              1 IACIGGPPNICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                    Tetraodon fluviatilis (Puffer fish).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Meopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.

NCBI_TaxID=47145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.
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                                               Length 785
                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307106; AAL09415.1; -.
HSSP; 942227; 18G1.
                  89643 MW; 81F231BDB27DE938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87411 MW; E661FFE18BEFD8BE CRC64;
                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                              Score 635; DB 2;
Pred. No. 7.2e-51;
4; Mismatches 4;
                                                                                                                                                                                                                                                                                764 AA.
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Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
SMART; SM00252; SH2; 1.
                                               94.9%;
Pfam; PF02865; STAT int; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 785 AA; 89643 MW
                                            Query Match
Best Local Similarity 93.8°
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 92.2
Matches 119; Conservative
                                                                                                                                                                                                                                                                                PRELIMINARY;
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DKESGDVAA 378
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DKESGDVAS 378
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PROSITE; PS50001;
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Q90Y16
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RESULT 15 013133

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250 IACIGGPPKICLDRLETWITSLGEIQLQIRQQIKKLEELQQKVSYKGDPIIQHRPALEEK 309
                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; 1060331; ABB60926.1; -.

REMBL; 1060331; ABB60926.1; -.

ROS; GO:0004371; F:signal transderrighter activity; IEA.

GO; GO:0003710; F:transcription factor activity; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0003755; P:requlation of transcription, DNA-dependent; IEA.

ROS; GO:0000375; P:sintracellular signaling cascade; IEA.

GO; GO:0000375; P:transcription of transcription, DNA-dependent; IEA.

ROS; GO:0000370; FROO0980; SH2.

R InterPro; IPRO00980; SH2.

R Pfam; PF00017; STAT alpha; 1.

R Pfam; PF02017; STAT alpha; 1.

R Pfam; PF02865; STAT int; 1.

R Pfam; PF02865; STAT int; 1.

R Pfam; PF02865; STAT int; 1.
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                                                                                                                                Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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89.7%; Score 600; DB 2; Length 767;
Best Local Similarity 89.9%; Pred. No. 1.3e-47;
Matches 116; Conservative 4; Mismatches 9; Indels
                                    Last sequence update)
Last annotation update)
      Created)
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   01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-MAR-2004 (TrEMBLrel. 26,
(TrEMBLrel.
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Mouse

sig ISG exp Sta STA Sta

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Rat STAT-
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/note= "Stat3-c-Jun interaction region 2; corresponds to
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is mouse Stat3 protein fragment containing 282-377 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A
                                                                                                                                                                                                                                                                                                Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                           Human
84 kD
                                                                                                                            Human
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Human
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                         Aay72862
Aay72846
Aay72860
Aay72851
Aay72847
Aag78526
                                                                                   Aaw62996 I
Abu04748 I
Adh57036 I
Abr59713 I
Aar41335 Abu04741 I
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Abu04747
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                                                                                                                                                                                                                                                                                 Mouse Stat3 protein fragment #15 (282-377 amino acids)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Darnell JE;
                                                                                                                                                                                      ALIGNMENTS
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                                AAY72846
AAY72860
AAY72861
AAY72861
AAY72867
AAG786296
ABG8296
ABU04748
ABRS 9713
AAR71335
AAR720731
AAR720731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 65; Page 81; 86pp; English
                                                                                                                                                                                                                               AAY72857 standard; protein; 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00387418.
                                                                                                                                                                                                                                                                 (first entry)
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WPI; 2001-226705/23.
WO200116605-A2
                                                                                                                                                                                                                                                                31-MAY-2001
                                                                                                                                                                                                                                                                                                                                   Mus musculus
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AAY72857;
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                                                     May 25, 2005, 17:14:45 ; Search time 51.0983 Seconds (without alignments) 726.619 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Ab57164
Aac22055
Aar82995
Aay03776
Aay03776
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Aay03776
Aay03776
Aay04462
Aay04462
Adb64434
Aab684749
Aab646744
       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                   2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                             Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                    AAY72856
AAY72855
AAY72854
AAY72841
AAE22055
ABE57164
AAE22056
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AAE22056
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AAY03768
AAB12377
AAE14652
ABG69497
ABU10476
ADN04365
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ADD44738
AAR82993
AAB19964
AAE15174
ADD44740
                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                              geneseqp1998s;
geneseqp200s;
geneseqp2001s;
geneseqp2002s;
geneseqp2003as;
                                                                                                                                                                                                                                                Geneseq_16Dec04:*
geneseqp1980s:*
                                                                                                                                                                                                                                                                                                                 geneseqp20048:*
                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                          US-10-090-185-25
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Match Length
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Result Š.

Post-processing:

Database

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Gaps

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Mismatches

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  96;
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Region
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AAY72855
ID AAY7285
ID AAY785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse, Stat3 protein, transcription factor, c-Jun, gene transcription, cellular transformation, dysproliferative disease, cancer, psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94. .110
/note= "Stat3-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
                                                                                                                                                                                                 1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                                                                                                                                                                                                                                          KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for use in modulating the interaction between c-Jun and a Stat3 protein.
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Pred. No. 5.2e-55;
                                                                                                          Length 96,
                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse Stat3 protein fragment #14 (249-377 amino acids)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Darnell JE;
                                                                                                        ; Score 494; DB 4;
; Pred. No. 3.6e-55;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                       GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wrzeszcynska MH,
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                                                                                                      Query Match
Best Local Similarity 100.
Matches 96; Conservative
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transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang X, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-226705/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                    Sequence 96 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is mouse Stat3 protein fragment containing 193-377 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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  9
                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150. .166
/note= "stat3.c-Jun interaction region 2; corresponds to
342-258 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                            34 KKLEELQQXVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPVIKT
1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Stat3 protein fragment #13 (193-377 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Darnell JE;
                                                                                                                100.0%; Score 494; DB 4;
100.0%; Pred. No. 8.4e-55;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wrzeszcynska MH,
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                                                                                                                                                                                                                                                                                                                      AAY72855 standard; protein; 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-2000; 2000WO-US023822
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
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AAY72854;

therapy.

Key Region

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236. .252
/note= "Stat3-c-Jun interaction region 2; corresponds to
342-358 position of Stat3 protein"
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                                                                                                                                                                                                                                                                                                   /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"
                                                                                                                                           Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
                                                                                                      Mouse Stat3 protein fragment #2 (107-377 amino acids).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 494; DB 4;
100.0%; Pred. No. 1.4e-54;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang X, Horvath C, Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 65; Page 67-68; 86pp; English.
                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                 (first entry)
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Best Local Similarity
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                                                                 31-MAY-2001
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                          AAY72841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is mouse Stat3 protein fragment containing 155-377 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                               Mouse, Stat3 protein, transcription factor, c-Jun; gene transcription, cellular transformation, dysproliferative disease, cancer, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                               corresponds
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                                                                                                                                                                                                                                                                                                                                                                                                                         188. .204
/note= "Stat3-c-Jun interaction region 2;
342-358 position of Stat3 protein"
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                                                                                                                                                                                                                                          Mouse Stat3 protein fragment #12 (155-377 amino acids).
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100.0%; Score 494; DB 4;
100.0%; Pred. No. 1.1e-54;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVOFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 223
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188. .204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 65; Page 79; 86pp; English
                                                                                                                       AAY72854 standard; protein; 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-2000; 2000WO-US023822
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tes 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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Zhang X,

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RESULT 5 AAY72841 ΩI

Query Match

Best Loc Matches

Length 271; Indels Stat3beta protein

Sequence 720 AA;

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Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vacular occlusion; hypostais stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; prolliferative angiopathy; autoimmune thyroiditis; sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; prolliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion; Statbeta.
25-JUL-2002 (first entry)
                                                                                                              Human Stat3beta protein.
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Homo sapiens

Key Location/Qualifiers Misc-difference 713. .714 /note= "Encoded by ACA CCA ITC"

WO200220032-A1

14-MAR-2002

10-SEP-2001; 2001WO-US028254.

08-SEP-2000; 2000US-0231212P

(UYSF-) UNIV JOHNS HOPKINS.

Jove R, Dalton W; ru H, Pardoll D,

WPI; 2002-362218/39. N-PSDB; AAD35066.

Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator transcription 3.

Disclosure; Page 87-89; 94pp; English

The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, mycardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, croclusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hyposlyvaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy citrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy introgen necrosis, proliferative angiopathy e.g. diabetic microangiopathy amplibration Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus erythematogus, multiple sclerosis, insulin dependent diabetes mellitus, caleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, insulin dependent diabetes mellitus, caleroderma, polymyositis, chronic active hepatitis, caleroderma, polymyositis, chronic active hepatitis, cithopathic thrombocytopenia purpura, Grave's disease, rheumatoid arthritis, cirhosis, pemphigus vulgaris, autoimmune collitis and disease, theumatoid arthritis, cirhosis, pemphigus vulgaris, autoimmune collitis, disease, prominer active and oncogenic disease which includes sarcomas and carcinomas equiperior and oncogenic disease which includes sarcomas and carcinomas equiperior properior phypoproliferative disercinoma, degenerative disease physical trauma, lesions and wounds. The method is used in gene therapy. The present sequence is human

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR thargeutics for ischaemic condition related sequence, which are used in the exemplification of the present invention

Claim 2; Page 1084-1087; 2690pp; English.

Score 494; DB 5; Length 769; Pred. No. 5.3e-54;

100.0%;

Query Match Best Local Similarity

Sequence 769 AA;

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                                                          282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 341
                                             1 KKLEBLQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                       Gaps
                                                                                                                                                                                                                                              Mouse ischaemic condition related protein sequence SEQ ID NO:398
                       .;
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                                                                                                                                                                                                                                                                     Mouse, ischaemia, compressive ischaemia, occlusive ischaemia, vasospastic ischaemia, ischaemic condition, ischaemic disease.
Length 720;
                       Indels
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                                                                                                        GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
100.0%; Score 494; DB 5;
100.0%; Pred. No. 4.8e-54;
iive 0; Mismatches 0;
                                                                                           GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
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                                                                                                                                                                            ABB57164 standard; protein; 769 AA.
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                       96; Conservative
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                          Mus musculus.
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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, inche lower extremities, infarction, inflammation, issue ischaemia in the lower extremities, infarction, tranma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, itrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
                                                             282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHDRPLVIKT 341
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                                        1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy, polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; arcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest;
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(UYSF-) UNIV SOUTH FLORIDA.
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96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         Human Stat3 protein.
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              anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human Stat3
  scleroderma, polymyositis, chronic active hepatitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.
                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                          100.0%; Score 494; DB 5; Length 769; 100.0%; Pred. No. 5.3e-54; ive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 GVQFTTKVRLLVKFPELAYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein related to angiogenesis regulation.
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Zhong Z;

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A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080) (Stat1) that was responsive to interferon-gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AAQ89339-440) were cloned in plasmids 13sfl and 19sf6 and encoded proteins termed Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMFDRPLVIKT 341
                                                                                                                                                                                                                                                                      Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.
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100.0%; Pred. No. 5.3e-54;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 107-110; 160pp; English.
                                                                                                                                       Shuai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR82995 standard; protein; 770 AA
  94US-00212184.
94US-00212185.
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                                                                                                                                    Schindler CW,
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N-PSDB; AAQ89340.
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11-MAR-1994;
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                                                                                                                                    Darnell JE,
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                                                                                          The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription of Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemia condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, trauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus eythematosus, multiple sclerosis, insulin dependent diabetes mellitus, slogern's syndrome, scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary circhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's disease, themmacoid arthritis, circhosis, pemphigus vulgaris, autoimmune cure deposit disease. The method is useful in preventing or treating appropriation archivement carring and cense deposit disease. The method is useful in preventing or treating appropriation archivement carring and cense deposit disease and consequence of accidence archivers and accidence archive and accidence archive and accidence archive and accidence archive and accidence archives and accidence archive and accidence archives and accidence and accidence archives.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal transducer and activator of transcription; STAT; 19sf6; Stat3; receptor recognition factor; transcription factor; cellular debilitation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GVQFTTKVRLLVKFPELNYQLKIKVCIDXDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein related to angiogenesis regulation
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                                                  Disclosure; Page 83-85; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR72082 standard; protein; 770 AA.
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93US-00126595
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24-SEP-1993;
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27-SEP-1995
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Length 770; 0; Indels ö

Length 770;

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STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from ligand-activated receptor kinase complexes followed by nuclear translocation and DNA binding to activate transcription. Recombinant STAT4 can be obtd. using cDNA clone 19sf6 (AAT31278) obtd. from splenic/thymic cells. STAT4 includes a DNA-binding domain (see also AAW03167) capable of both receptor recognition and message delivery vi DNA binding in a receptor-ligand specific manner. STAT proteins and the binding domains (see also AAW03165-75) are useful for screening antagonists used to inhibit STAT-mediated signal transduction and activation of transcription
                                                                                                                                                                                                                  1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                                                                                                                                                                                                                                                                                342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                                100.0%; Score 494; DB 2;
100.0%; Pred. No. 5.3e-54;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                  GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                           Local Similarity 100.
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N-PSDB; AAX29281.
                                                                                                                                        Sequence 770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
                                                          The sequence represents a mouse acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (I) of the protein is encoded by a cDNA, isolated from a mouse liver CDNA library using a polymerase chain reaction product (amplified using primors derived from an IL-6-treated mouse liver peptide) as a probe. APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or riboxymes, may be used to treat diseases induced by IL-6, e.g. inflammatory disease, leukemia, cancer, osteoclasia, pulmonary

    useful for diagnosing,
    oncogenesis,

                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   und binding profein; ligand; receptor; oncogenesis; inflammation; autoimmune disease; antagonist; therapy.
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                                                                                                                                                                                                               Length 770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New STAT protein DNA-binding domain peptide(s) - u preventing or treating cellular dysfunction, e.g. inflammation, parasitic disease or autoimmunity.
                                                                                                                                                                                                               Score 494; DB 2;
Pred. No. 5.3e-54;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                GVOFTTKVRLLVKFPELNYQLKIKVCIDKOSGDVAA 377
                                                                                                                                                                                                                                                                                                                   GVOFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398. .508
/label= DNA binding domain
/note= "Claim 3, page 110"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 87-90; 138pp; English.
                                     Page 20-22; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wen Z, Horvath CM,
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                                                                                                                                                                                                             Query Match
Best Local Similarity 100.'
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-333941/33
                                                                                                                                                                  hypertension, etc
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                                                                                                                                                                                        Sequence 770 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse STAT4
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                                     Claim 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW03176;
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Domain
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The present sequence represents a predominant allelic variant of human Signal Transducer and Activator of Transcription 3 (STAT3) protein, an intracellular transcription factor which mediates IL-6 signals. The encoding sequence differs from the original published human STAT3 gene DNA molecule can be used for the recombinant expression of the variant. STAT3 protein is useful as a medicament or pharmaceutical composition for treatment of autoimmune or inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                  Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6; intracellular transcription factor; interleukin-6; medicament; variant; pharmaceutical; autoimmune disease; inflammatory; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human Signal Transducer and Activator of Transcription 3 (STAT3) allelic variant useful for treatment of autoimmune and inflammatory
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AAY03768 standard; protein; 770 AA.
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                                                                                                                                                                                                                                                                            Human STAT3 allelic variant
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                                                 282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 341
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                                     1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                     Gaps
                                                                                                                                                                                                                  STAT; signal transducer and activator of transcription; crystal; drug design; murine.
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 Length 770;
                    0; Indels
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                                                                                    1100.0%; Score 494; DB 2;
100.0%; Pred. No. 5.3e-54;
ive 0; Mismatches 0;
                                                                         GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                 N-terminal domain of murine STAT-3 protein.
                                                                                                                                                                                                                                                                                                            19...21
/label= 3(10) helix of a. 28...33
/label= Alpha helix 3
35..40
/label= Alpha helix 4
43...47
/label= Alpha helix 5
50...73
/label= Alpha helix 6
77...96
/label= Alpha helix 6
77...96
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/label= Alpha helix 1
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|abel= Alpha helix 2
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/label= Alpha helix 8
                                                                                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                         AAB12377 standard; peptide; 770 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening and development
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                   96; Conservative
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          Similarity
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than 5.0 Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to methods for detecting compounds that bind to signal transducer and activator of transcription (STAT) proteins for the discovery and development of new drug compounds based on the structural properties of the protein crystal. The methods include: identifying a compound that binds to the N-terminal domain of a STAT protein, compound that binds to the networks or diminishes the binding of the dimeric STAT proteins to each other and/or their nucleic acid binding site; or identifying a compound that enhances or diminishes the ability of STAT protein dimers to induce the expression of a gene operably under the control of a promoter containing at least two adjacent weak binding sites for STAT protein dimers. The methods are used for identifying new

    .130
/note= "Conserved N-terminal domain of the STAT family"

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                                                                                                                                                                   Length 770;
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                                                                                                                                                               100.0%; Score 494; DB 3;
100.0%; Pred. No. 5.3e-54;
ive 0; Mismatches 0;
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                                                                                                                                                                                  Similarity 100.0%; 96; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine STAT3 protein.
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                                                                                                                               Sequence 770 AA;
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The present invention relates to a crystal of an N-terminal fragment of signal transducer and activator of transcription (9747) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater

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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-387-418A-29
US-09-387-418A-9
US-08-92-796-12
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US-08-92-796-12
US-08-95-652-12
US-08-95-652-12
US-08-95-652-12
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Sequence 24, Application US/09387418A

Patent No. 6391572

GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: MITCANT: APPLICANT: Horvath, Curt M

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

FILE REFERENCE: 600-1-253

CURRENT APPLICATION NUMBER: US/09/387,418A

CURRENT FILING DATE: 199-08-31

NUMBER OF SEQ ID NOS: 43
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US-09-387-418A-18
US-09-387-418A-28
US-09-387-418A-30
US-09-387-418A-31
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US-09-387-418A-19
US-09-387-418A-12
US-09-387-418A-12
US-09-387-418A-12
US-08-369-796-6
US-08-852-091-6
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US-08-956-652-6
US-08-956-653-6
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APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Barnall Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-223
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 199-08-31
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.
Matches 96; Conservative
  TYPE: PRT
ORGANISM: Mus musculus
US-09-387-418A-25
  RESULT 2
US-09-387-418A-24
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Sequence 9, Application US/09387418A
Sequence 9, Application US/09387418A
Sequence 9, Application US/09387418A
GENERAL INFORMATION:
APPLICANT: Clang, Xiaokui
APPLICANT: Horvath, Curt M
APPLICANT: NERRIOS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: NUMBER: US/09/387,418A
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: James B.
APPLICANT: Zilong Wen
APPLICANT: Zilong Wen
APPLICANT: Zilong Wen
APPLICANT: Zilong Zilong Wen
APPLICANT: Zilong Zil
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100.0%; Pred. No. 1.3e-53;
iive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.7e-53;
Matches 96; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 96; Conservative
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TYPE: PRT
ORGANISM: Mus musculus
                                                           ; ORGANISM: Mus musculus
US-09-387-418A-22
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US-08-369-796-12
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US-09-387-418A-9
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Sequence 22, Application US/09387418A
GENERAL INFORMATION:
APPLICANT: Waresaczynska, Melissa H
APPLICANT: Darnell Jr., James B
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 223
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APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Dr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 185
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; Sequence 23, Application US/09387418A
; Patent NO. 6391572
; GENERAL INFORMATION:
                                    PatentIn Ver. 2.0
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; ORGANISM: Mus musculus
US-09-387-418A-23
                                                                                                                                                                         ORGANISM: Mus musculus US-09-387-418A-24
SOFTWARE: Pate
SEQ ID NO 24
                                                                                                                                        TYPE: PRT
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Sequence 12, Application US/08852091

Sequence 12, Application US/08852091

Patent No. 588328

GENERAL INFORMATION:

APPLICANT: James E. Darnell, Jr.

APPLICANT: Curt M. Horvath

APPLICANT: ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                            282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 341
                                                                                                                                                                                                                                                          1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
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                                                                                                                                                             Length 770;
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                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                      342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                        100.0%; Score 494; DB 1;
100.0%; Pred. No. 6.4e-53;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            61 GVOFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
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Pred. No. 6.4e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; P:
Matches 96; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
     : 770 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             Best Local Similarity 100.
Matches 96; Conservative
                                                                        MOLECULE TYPE: protein US-08-416-5818-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-852-091-12
                                                   TOPOLOGY: linear
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                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 60
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100.0%; Pred. No. 6.4e-53;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08416581B
Fatent No. 5719042
GENERAL INFORMATION:
APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Akira, Shizuo
ITILE OF INVENTION: TRANSCRIPTION FACTOR APRF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:

MEDIUW TYPE: Ploppy disk
COMPUTER: IBM PC compatible
ORPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/16,581B
FILING APPLICATION NUMBER: US/08/16,581B
FILING APPLICATION NUMBER: US/08/16,581B
FILING APPLICATION NUMBER: US/08/16,581B
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GVOFTTKVRLLVKFPELNYOLKIKVCIDKDSGDVAA 96
                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
TELEX: 133521
TELEX: 133521
TELEX: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: NAKamura, Dean H.
REGISTRATION NUMBER: 33,981
REGISTRATION NUMBER: 0-37891
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                            PC-DOS/MS-DOS
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                          i LENGTH: 770 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-369-796-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 96; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-416-581B-9
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61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
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                                                                                                                                                                                                                                                                                                            APPLICANT: Schindler, Christian W. APPLICANT: Schindler, Christian W. APPLICANT: Schindler, Christian W. APPLICANT: Schindler, Christian W. APPLICANT: Fu, Xian-Yuan APPLICANT: Wen, Zilong APPLICANT: Zhong, Zhong Zhong TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Alauber & Jackson STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
RILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 11-MAR-1992
RILING DATE: 11-MAR-1992
RILING DATE: 11-MAR-1992
RILING DATE: 19-MAR-1992
RILING DATE: 19-MAR-1992
RILING DATE: 19-MAR-1993
RILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: 20-KSEP-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 20,742
REFERENCE/DOCKET NUMBER: 20,742
RELEEPHONE: 201 487-5800
                                                                   342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                     61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                          Sequence 12, Application US/08820754
Patent No. 5976835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                         US-08-820-754-12
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282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 341

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1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
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                                                GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
APPLICANT: Wen, Zilong
APPLICANT: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
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100.0%; Score 494; DB 3;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEFHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/999,032
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 12-MAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-5EP-1993
ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT PROPARATION:
ATTORNEY AGENT PROPARATION:
Sequence 12, Application US/08956652
Patent No. 6013475
                                                                                                                                                                                                                                                                                                                                            STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 770 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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US-08-948-547-12
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100.0%; Score 494; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels (
                                                                                                                                    Sequence 12, Application US/08956869
Patent No. 6030808
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Fu, Xian-Yuan
APPLICANT: Pong, Zhong
APPLICANT: Zhong
APPLICANT: SEGUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 07601

ZIP: 07601

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,869
342 GVOFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 083/02569
FILING DATE: 19-MAR-193
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNIMKSAFVVERQPCMPMHPDRPLVIKT 341
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Sequence 8, Application US/09012710
| Patent No. 6087478
| GENERAL INFORMATION:
| APPLICANT: Vinkemeier, Uwe | APPLICANT: Worzefi, Ismail | APPLICANT: Waristan, John | TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 13
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 494; DB 3; Length 770; 100.0%; Pred. No. 6.4e-53; ive 0; Mismatches 0; Indels
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Patent No. 6124118
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Darmell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Tong, Zhong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
FILING DATE:
CLASSIFTCATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5801
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                                                                                                                                                                                                                          STREET: ALUDRESS:
STREET: All Hackensack Avenue, 4th Floor
CITY: Hackensack
STREE: New Jersey
COUNTRY: USA
ZIP: 07601
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Best Local Similarity 100.0
Matches 96; Conservative
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STRANDEDNESS: single
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Query Match
Best Local Similarity 100.0
Matches 96; Conservative
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; ORGANISM: Mus musculus
US-09-364-970-5
SEQ ID NO 3
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
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LENGTH: 770
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TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORY
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REPERBUGE: 600-1-25
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT APPLICATION NUMBER: US/09/364,970
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                        ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
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100.0%; Score 494; DB 3;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION UNMBER: US 07/854,296
FILING DATE: 19-NAR-1992.
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-NAR-1993
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-NAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEF-1993
ATTORNEY ARENT INFORMATION:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEF-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09364970 Patent No. 6235873 GENERAL INFORMATION:
    CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 770 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-948-547-12
                                                                                               STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPWHPDRPLVIKT 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Jacqueline
TITLE OF INVENTION:
CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
FILE REFERENCE: 600-1-25
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTI VET: 2.0
                                                                                                         1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
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  Length 770;
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100.0%; Score 494; DB 3;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0;
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100.0%; Score 494; DB 3;
100.0%; Pred. No. 6.4e-53;
iive 0; Mismatches 0;
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; Sequence 5, Application US/09364970
; Patent No. 6235873
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May 25, 2005, 17:36:58; Search time 42.0417 Seconds (without alignments) 763.830 Million cell updates/sec
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494
1 KKLBELQQKVSYKGDPIVQH......LNYQLKIKVCIDKDSGDVAA 96
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1: /cgn2_6/ptodata/2/pubpaa/USO7_bUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_bUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1434725 seqs, 334507595 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                             OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Semience 12
ID	US-10-090-185-25	US-10-090-185-24	US-10-090-185-23	US-10-090-185-22	US-10-090-185-9	US-10-380-020-4	US-10-380-020-2	US-10-380-020-5	US-09-876-773-12	US-10-045-792-8	US-10-038-010-56	US-10-117-087-2	115-10-639-617-12
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% Query Match Length DB	96	129	185	223	271	720	169	169	770	770	770	770	770
* Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	494	494	494	494	494	494	494	494	494	494	494	494	494
Result No.	-	7	٣	4	S	9	7	89	6	10	11	12	13

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Length 96; Indels

th 100.0%; Score 494; DB 13; Similarity 100.0%; Pred. No. 2.9e-53; 96; Conservative 0; Mismatches 0;

Query Match Best Local Similarity Matches 96; Conserv

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RESULT 1 US-10-090-185-25 Sequence 25. Application US/1009018; Publication No. US20020197647A1; GENERAL INFORMATION: APPLICANT: Tanag, Xiaokui APPLICANT: Tanag, Xiaokui APPLICANT: Hyrzeszczynska, Melissa APPLICANT: Darnell Jr., James E TITLE OF INVENTION: METRACTIONS; TITLE OF INVENTION: METRACTIONS; FILE REFERENCE: 600-1-253 CURRENT FILING DATE: 1999-08-31 CURRENT FILING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 43 SOFTWARE: PRECENTING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 43 SOFTWARE: PRECENTING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 43 SOFTWARE: PRECENTING DATE: 1999-08-31 UNIMBER OF SEQ ID NOS: 43 SOFTWARE: PRECENTING DATE: 2.0 SEQ ID NO 25 TENGTH: PRECENTING DATE: 2.0 SEQ ID NO 25 TENGTH: PRECENTING DATE: 2.0 SEQ ID NO 25 TENGTH: PRECENTING DATE: 2.0 SEQ ID NO 25 UNIMBER OF SEQ ID NOS: 43 SOFTWARE: PRECENTING DATE: 2.0 SEQ ID NO 25 UNIMBER OF SEQ ID NOS: 43 SOFTWARE: PRECENTING DATE: 2.0 SEQ ID NO 25 UNIMBER OF SEQ ID NOS: 43 SOFTWARE: PRECENTING DATE: 2.0 SEQ ID NO 25 UNIMBER OF SEQ ID NOS: 43 SOFTWARE: PRECENTING DATE: 2.0 SEQ ID NO 25 UNIMBER OF SEQ ID NOS: 43 SOFTWARE: PRECENTING DATE: 2.0 SEQ ID NO 25 UNIMBER OF SEQ ID NOS: 43 SOFTWARE: PRECENTING DATE: 2.0 SEQ ID NO 25 UNIMBER OF SEQ ID NOS: 43 SOFTWARE: PRECENTING DATE: 2.0 SEQ ID NO 25 UNIMBER OF SEQ ID NOS: 43 SOFTWARE: PRECENTING DATE: 2.0 SEQ ID NO 25 UNIMBER OF SEQ ID NOS: 43 SOFTWARE: PRECENTING DATE: 2.0 SEQ ID NO 25 UNIMBER OF SEQ ID NOS: 43 SOFTWARE: PRECENTING DATE: 2.0	LUT 1 10-090-185-2 10-090-185-2 10-090-185-2 10-090-185-2 10-090-185-2 10-090-185-2 10-090-185-2 10-090-185-2	SULT 1 -10-090-185-25 Sequence 25, Application US/10090185 Sequence 26, Application US/10090185 GENERAL INFORMATION: APPLICANT: Abang, Xiaokui APPLICANT: Abang, Xiaokui APPLICANT: Abang, Xiaokui APPLICANT: Horzesczynska, Melissa H APPLICANT: USTER EN	tion US/100901 2020197647A1 iaokui 'Yanska, Meliss 'Yurt M Jr., James E METHODS FOR I INTERACTIONS -1-253 NUMBER: US/10 : 2009/387, 1999-08-31 S: 43	Me.	H ENTIFYING MODULATORS OF 390,185 18	TRANSCRIPTIONAL ACTIVATOR

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APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James B
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: UNMERR: US/10/090,185
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID MOS: 43
SOFTWARE: PATENTIN VET. 2.0
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APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Curh
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
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Pred. No. 8.5e-53;
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CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
                                              Sequence 22, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 9, Application US/10090185; Publication No. US20020197647A1; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 96; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
US-10-090-185-22
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 22
LENGTH: 223
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                                                                                                                 APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR ITITLE OF INVENTION: INTERACTIONS
FILE REPERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT PILING DATE: 2002-03-04
FRIOR APPLICATION NUMBER: 09/387,418
FRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
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Publication No. US20020197647A1
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Mrzeszczyneka, Melissa H
APPLICANT: Mrzeszczyneka, Melissa H
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE OF INVENTION: INTERACTIONS
FILE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-233
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
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                    Sequence 24, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
TENGTH: 185
                                                                                                  APPLICANT: Zhang, Xiaokui
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US-10-090-185-23
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US-10-090-185-24
-10-090-185-24
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236 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271

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APPLICANT: YU, Hua
APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: 406/10/380,020
CURRENT FILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Publication No. US20040058318A1
GENERAL INFORMATION:
APPLICANT: Darnell dr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                    ; Sequence 5, Application US/10380020; Publication No. US20040052762A1; GENERAL INFORMATION:
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-5
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US-10-380-020-5
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                                                                                                 SERVICANT: YU, Huan APPLICANT: Pardoll, Drew APPLICANT: Pardoll, Drew APPLICANT: Pardoll, Drew APPLICANT: Dalton, Willian APPLICANT: Dalton, Willian TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof FILE REFERENCE: 10873-009-999 CURRENT APPLICATION NUMBER: 108/13-007-078 CURRENT FILING DATE: 2003-03-07 PRIOR APPLICATION NUMBER: 60/231,212 PRIOR APPLICATION NUMBER: 60/231,212 PRIOR FILING DATE: 2000-09-08 SOFTWARE: Patentin version 3.0 SEQ ID NO 4 LENGTH: 720
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Publication No. US20040052762A1
GENERAL INFORMATION:
APPLICANT: Pardoll, Drew
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
CURRENT FILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 494; DB 15; 100.0%; Pred. No. 3.8e-52;
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                                      Sequence 4, Application US/10380020
Publication No. US20040052762A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
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US-10-380-020-2
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                 US-10-380-020-4
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Length 770;

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| Sequence 56, Application US/10038010 |
| Publication No. US2030040089A1 |
| Publication No. US2030040089A1 |
| GENERAL INFORMATION |
| APPLICANT: HYBRIGENICS |
| APPLICANT: Pierre, Legrain |
| TILLE OF INVENITON: Protein-protein interactions in adipocyte cells |
| FILE REFERENCE: B4767A |
| CURRENT APPLICATION NUMBER: US/10/038,010 |
| PRIOR APPLICATION NUMBER: US 60/259,377 |
| PRIOR FILING DATE: 2001-01-02 |
| NUMBER OF SEQ ID NOS: 67 |
| SEQ ID NO 56 |
| LENGTH: 770 |
| LENGTH: 770 |
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Publication No. US20030166854A1

GENERAL INFORMATION:
APPLICANT: SERLUPI-CRESCENZI, Ottaviano
APPLICANT: DELLA PIETRA, Linda
TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
FILE REFERENCE: SERLUPI-S:
CURRENT APPLICATION NUMBER: US/10/117,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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100.0%; Pred. No. 4.2e-52;
iive 0; Mismatches 0;
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                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: STAT3 : Transcription factor
LOCATION: (1)..(770)
OTHER INFORMATION:
                                                           LENGTH: 770 amino acids
                                                                               TYPE: amino acid
STRANDEDNESS: single
     INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 96; Conservative
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Matches 96; Conservative
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ORGANISM: Homo sapiens
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Darnell, Jr., James E.
Ruriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-Oct-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 494; DB 11; 100.0%; Pred. No. 4.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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                                                                                                                           NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-073 CIP TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
FILING DATE: -Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-5EP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

HOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12
                                                                                                                                                                                                                          TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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Publication No. US20030003563A1
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 770 amino acids TYPE: amino acid
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ADDRESSEE: Klauber &
                                                                                                                                                                                                                                                                        TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New Jersey
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Matches 96; Conservative
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Length 770;

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Sequence 780, Application US/09925302; Publication No. US20030064072A9; GENERAL INFORMATION:
      SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino ac
                                             'YPE: amino acid
                                                                  TOPOLOGY: linear
                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 96; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-10-639-617-12
; Sequence 12, Application US/10639617
; Publication No. US20050079543A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
sequences AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                         Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/639,617
FILING DATE: 12-Aug-2003
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                         100.0%; Score 494; DB 14;
100.0%; Pred. No. 4.2e-52;
tive 0; Mismatches 0;
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US/09/526,542
PRIOR FILING DATE: 2000-03-19
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New Jersey
                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
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                                                                                                                                            TYPE: PRT
ORGANISM: Human
                                                                                                    SEQ ID NO 2
LENGTH: 770
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282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 341
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                                                                                                                                                                     Gaps
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                                                                                                               Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 780, Application US/09925302
Fatent No. US20020044941A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
SOFTWARE: PALCHIN NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
SOFTWARE: PALCHIN VEY: 2.0
SOFTWARE: PALCHIN VEY: 2.0
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILE REFERENCE: PAJ04
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 793;
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                            100.0%; Score 494; DB 17; 100.0%; Pred. No. 4.2e-52;
                                                                                                                                                                                                                                                                                                                                  61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 494; 100.0%; Pred. No. 4
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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Query Match 100.0%; Score 494; DB 10; Length 793; Best Local Similarity 100.0%; Pred. No. 4.3e-52; Matches 96; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                              ; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780
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Search completed: May 25, 2005, 18:21:52 Job time: 43.375 secs.

0; Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 25, 2005, 17:24:07 ; Search time 9.0566 Seconds (without alignments) 1019.898 Million cell updates/sec

Title:

US-10-090-185-25 494 1 KKLEELQQKVSYKGDPIVQH......LNYQLKIKVCIDKDSGDVAA 96 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries Match 100% Maximum

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	-н	ISGF3 p91-related	DNA-binding protei	interferon-depende	gamma-interferon a	interferon alpha-i	interleukin-4-indu	mammary gland fact	mammary gland fact	transcription acti	mammary gland fact	DNA-Binding Protei	4-hydroxyphenylpyr	4-hydroxyphenylpyr	argininosuccinate	MRS1 protein - yea	ovarian abundant m	2-acylglycerophosp	alloantigen F - ra	hypothetical prote	C kinase 1 interac	fatty-acid-CoA lig	F protein - mouse	hypothetical prote	fatty-acid-CoA lig	complex I intermed	hypothetical prote	malate dehydrogena	hypothetical prote	
SUMMARIES	ΩI	149508	A54444	A46159	A56047	A46160	A54740	I49274	S54772 ·	G02317	S55527	157557	S32458	S32821	T06667	S48483	A48461	E71667	S32820	T29703	JC7167	AF1479	A60236	T25063	AC1119	T47250	T39082	DEBYMM	T30084	H89907
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d	Query Match	100.0	99.0	62.8	57.3	•	18.3	17.5	17.5	7	~	16.9	4	4		13.8	13.8	13.8	13.6	13.6	13.6		13.4	13.4	13.4		13.3			13.0
	Score	494	489	310	283	204	90.5	86.5	86.5	86.5	86.5	83.5	72	72	7.1	9	89	68	67	67	67	67	99	99	99	65.5	65.5	64	64	64
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translation elonga	perinuclear bindin	probable gtpase ac	meiotic recombinat	mevalonate kinase	dynamin-related pr	ribonucleoside red	beta-lactamase (EC	conserved hypothet	hypothetical prote	probable ABC trans	GAP-associated pro	hypothetical prote	60S RIBOSOMAL PROT	pre-B cell enhanci	proteinase, probab
T43892	A56486	T39954	T41126	S42088	T39373	B84389	PNBSL	A99345	T21556	C71182	A38218	B70042	T48076	S73433	B81056
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395	416	695	339	378	781	804	307	328	369	580	1493	191	256	451	451
12.9	12.8	12.8	12.7	12.7	12.7	12.7	12.6	12.6	12.6	12.6	12.6	12.4	12.4	12.4	12.4
63.5	63	63	62.5	62.5	62.5	62.5	62	62	62	62	62	61.5	61.5	61.5	61.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149508; 149509
R;Akira, S.; Nishilo, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su Coll 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr A;Reference number: A54444; MUID:94208062; PMID:7512451
                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: mRNA
p91-related transcription factor - mouse
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A; Residues: 1-770 <RES>

Across-references: UNIPROT: P42227; GB:L29278; NID:g476715; PIDN: AAA37254.1; PID:g47671 R;Raz, R.; Durbin, J.E.; Levy, D.E.
d. Biol. Chem. 269, 24391-24395, 1994
A;Title: Acute phase response factor and additional members of the interferon-stimulate A;Reference number: 149009; MUID:95014185; PMID:7523373
A;Accession: I49009
A;Status: preliminary; translated from GB/EMBL/DDBJ

A,Molecule type: mRNA A,Residues: 1-393,'M',395-700,702-770 <RE2> A,Cross-references: EMBL:U08378; NID:g473889; PIDN:AAA56668.1; PID:g473890 C,Genetics:

A,Gene: APRF C,Superfamily: human signal transducer and transcription activator STATSA

Gaps ö Length 770; Indels 100.0%; Score 494; DB 2; llarity 100.0%; Pred. No. 4.6e-46; Conservative 0; Mismatches 0; Local Similarity tes 96; Conserv Query Match Best Loc Matches

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282 KKLEBLQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 341 1 KKLEBLQQKVSYKGDPIVQHRPMLEBRIVELFRNLMKSAFVVBRQPCMPMHPDRPLVIKT ò 셤

342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKOSGDVAA 377 61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96 ઠે 셤

RESULT 2

DNA-binding protein APRF - human Cispecies: Homo sapiens (man) Cjate: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004 CjAccession: A54444 RjAkira, S.; Nieblio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka,.T.; Yoshida, K.; Succell 77, 53-71, 1994 A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr A;Reference number: A54444; MUID:94208062; PMID:7512451 A, Accession: A54444 Length 748;

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57.3%;
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                                                                                                                  53; Conservative
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RySchindler, C.; Fu, X.Y.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
RySchindler, C.; Fu, X.Y.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
RySchindler, C.; Fu, X.Y.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
RyTitle: Proteins of transcription factor ISGF53: one gene encodes the 91-and 84-kDa ISG
RyReference number: A46159; MUID:92366557; PMID:1502203
RyScaesion: A46159
RyScaesion
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A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in ea A;Reference number: A56047; MUID:94277038; PMID:8007943
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A;Residues: 1-748 <YAM>
A;Cross-references: UNIPROT:P42228; GB:U09351; NID:g509502; PIDN:AAA19692.1; PID:g509503
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Homo sapiens (man)
.Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
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A; Experimental source: HeLa cells
A; Note: sequence extracted from NGBI backbone (NGBIP:110818)
C; Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                            A, Cross-references: GDB:358950
A, Map position: 17421-17421
C;Superfamily: human signal transducer and transcription activator STATSA
C;Keywords: DNA binding; transcription factor
                                                                                                                  A; Cross-references: UNIPROT: P40763; GB: L29277; NID: 9475788; PID: 9475789
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 GVQFTTKVRLLVKFPELNYQLKIKVCIDXDSGDVAA.377
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Pred. No. 1.6e-45;
Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Best Local Similarity
Matches 58; Conserv
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Best Local Similarity
                                                                              A; Residues: 1-770 < RES>
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Ciprecises: Home sapients (main)
Ciprecises: Addition; States (main)
Ciprecises: Addition; States (main)
Ciprecises: Main and the following of 18640-7843, 1992
Ciprecises: The proceises of 1868-3, the interferon alpha-induced transcriptional activator A;Reference number: Addition; Mulb:92366558; PMID:1502204
A;Reference number: Addition; Mulb:92366558; PMID:1502204
A;Reference number: Addition; Mulb:92366558; PMID:1502204
A;Residuce: preliminary; protein
A;Residuce: 1-851 < FUID:
A;Residuce: 1-851 < FUID:
A;Residuce: Ciprecises: UNFROT:P52630
A;Note: sequence extracted from NCBI backbone (NCBIP:110820)
A;Note: sequence extracted from NCBI backbone (NCBIP:10820)
Ciprecises: Ciprecises: Men, Z.; Darnell, J.E.
Submitted to the EMBL Data Library, December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes: multiple exons in coincident sites in PMID:7885841
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A, Readidues: 1-681 - XRAN-
A), Cross-references: EMBL: U18671; NID: 91293919; PIDN: AAA98760.1; PID: 91293920
R, Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
Nucleic Acids Res. 23, 459-463, 1995
A, Fittle: The genomic structure of the STAT genes: multiple exons in coincider
A, Reference number: S53873; MUID: 95192056; PMID: 7885841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferon alpha-induced transcription activator ISGF-3, 113K chain - human
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; Score 283; DB 2;
; Pred. No. 6.1e-23;
15; Mismatches 22;
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44.4%; Pred. No. 3.3e-14;
tive 19; Mismatches 31;
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GSKFTVRTRLLVRLQEGNESLTVEVSIDRN 366
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A;Cross-references: EMBL:U18671
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NyAlternate names: stat5 protein
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: 854772; 149273
R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleuki
A;Reference number: 854772; MuID:95237198; PMID:7720707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:Z48538; NID:g758633; PIDN:CAA8 R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L. Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Itle: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved A;Reference number: 149273; MUID:96004632; PMID:7568026
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C;Superfamily: human signal transducer and transcription activator STAT5A
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C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02317
R;Lih, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: U21103; NID: 9747971; PIDN: AAA80590.1; PID: 9747972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-793 <MUI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 86.5; DB 2;
; Pred. No. 0.23;
15; Mismatches 26;
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Pred. No. 0.23;
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A;Molecule type: mRNA
A;Regidues: 1-793 <RES>
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A;Residues: 1-794 <LIN>
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MBO J. 14, 1166-1175, 1995
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A,Reference number: S54772, MUID:95237198; PMID:7720707
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A;Residues: 1-432, E', 434-786 <MUI>
A;Cross-references: BMEL:Z48539; NID:g758635; PIDN:CAA88420.1; PID:g758636
R;Azam, M.; Brdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris,
EMBO J. 14, 1402-1411, 1995
A;Title: Interleukin-3 signals through multiple isoforms of Stat5.
A;Reference number: S54725; MUID:95246733; PMID:7537213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NyAlternate names: STATE protein homolog p80
C;Species: Mus musculus (house mouse)
C;Date: 02-011-1996 #sequence revision 02-011-1996 #text_change 09-011-2004
C;Accession: 149274; S54773; S54727
R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stats and an additional homologue (Stat5b) involved
A;Reference number: 149273; MUID:96004632; PMID:7568026
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                                                                                                                                A;Accession: A54740
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-848 (HOU)
A;Cross-references: UMIPROT:P42226
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription regulation
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Science 265, 1701-1706, 1994
A;Title: An interleukin-4-induced transcription factor: IL-4 stat.
A;Reference number: A54740; MUID:94367369; PMID:8085155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.3%; Score 90.5; DB 2; Length 8 36.2%; Pred. No. 0.091; cive 12; Mismatches 23; Indels
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A;Molecule type: mRNA
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A,Residues: 1-432,'E',434-786 <AZA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 36.2%
Matches 25; Conservative
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A;Molecule type: protein
A;Residues: 83-118;151-174;194-196;198-224;230-254;256-265;267-273;341-356;358-361;370-
R;Endo, F.; Awate, H.; Tanoue, A.; Ishiguro, M.; Eda, Y.; Titani, K.; Matsuda, I.
submitted to the EMBL Data Library, October 1992
A;Description: Primary structure deduced from complementary DNA sequence and expression:
A;Reference number: S35889
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A;Residues: 1-120, 'EVCCAADVRGHHTPLDRARQVWBG',145-150,'TFCLDSR',158,'QPSQTLLHRL',169-393|
A;Cross-references: EMBL:D13390; NID:g217691; PIDN:BAA02660.1; PID:g217692
C;Superfamily: 4-hydroxyphenylpyruvate_dioxygenase
C;Keywords: homodimer; oxidoreductase
C;Species: Homo sapiens (man)
C;Date: 28-May-1993 #sequence_revision 02-Jun-1994 #text_change 12-Jul-2004
C;Date: 28-May-1993 #sequence_revision 02-Jun-1994 #text_change 12-Jul-2004
C;Accession: 333458; 840298; S31153
R;Rueeteschi, U.; Dellsen, A.; Sahlin, P.; Stenman, G.; Rymo, L.; Lindstedt, S.
Eur. J. Biochem. 213, 1081-1089, 1993
A;Title: Human 4-hydroxyphenylpyruvate dioxygenase. Primary structure and chromosomal 1
A;Reference number: S32458; MUID:93279307; PMID:8504803
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 2-23;41-76;82-108;119-142;151-162;167-179;181-217;221-268;271-300;302-310;3
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 12-Jul-2004
C;Accession: S23821; S35890; S3589
B;Endo, F; Awata, H; Tanoue, A.; Ishiguro, M.; Eda, Y.; Titani, K.; Matsuda, J. Biol. Chem. 267, 24235-24240, 1992
A;Title: Primary structure deduced from complementary DNA sequence and expressientical subunits homologous to rat liver-specific alloantigen F.
A;Reference number: S32821; MUID:93077502; PMID:1339442
                                                                                                                                                                                                                                                      A;MOJecule type: mRNA
A;Residues: 1.393 <RU1>
A;Residues: 1.393 <RU1>
A;Cross-references: UNIPROT:P32754; EMBL:X72389; NID:g288104; PIDN:CAA51082.1;
A;Note: the authors did not translate the codon for residue 1
A;Accession: S40298
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C,Superfamily: 4-hydroxyphenylpyruvate_dioxygenase
C,Keywords: homodimer; oxidoreductase
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14.6%; Score 72; DB
Best Local Similarity 24.4%; Pred. No. 4;
Matches 22; Conservative 17; Mismatches
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A;Residues: 1-33 <END1>
A;Cross-references: UNIPROT:Q02110; EMBL:D13390
A;Accession: 835890
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A;Gene: GDB:HPD; PPD
A;Cross-references: GDB:135978; OMIM:276710
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                                                                                                                                                                                                                               the cytokine regula
                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-794 <WAK.>
A; Residues: 1-794 <WAK.>
A; Cross-references: UNIPROT: P42231; EMBL: X78428; NID: 9602354; FIDN: CAA55191.1; PID: 96023
A; Note: this is a revision to the sequence from reference 544353
EMBO J. 13, 2182-2191, 1994
A; Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcri
A; Réference number: $44353; MUID: 94244619; PMID: 7514531
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                                mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: S5527; 844353
R;Wakao, H.; Gouilleux, F.; Groner, B.
R;Wakao, H.; Gouilleux, F.; Groner, B.
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cyt
A;Reference number: S55527; MUID:95188889; PMID:7882987
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A,Gene: STAT6
C,Superfamily: human signal transducer and transcription activator STAT5A
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C;Superfamily: human signal transducer and transcription activator STAT5A
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Best Local Similarity 30.6%; Pred. No. 0.23;
Matches 22; Conservative 15; Mismatches 26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-716,'RHLHGPGSLPSR',729,'P',731,'ASL' <WAW>
A;Cross-references: EMBL:X78428
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A;Molecule type: mRNA
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33.3%; Pred. No. 0.52;
Live 15; Mismatches
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KVSYKGDPIV-----QHRPMLEERIVELF-RNLMKSAFVVERQPCMPMHPDRPLVIKT 60
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R;Kreike, J.; Schulze, M.; Ahne, F.; Lang. B.F.
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BMBO J. 6, 2123-2129, 1987
A;Title: A yeast nuclear gene, MRS1, involved in mitochondrial RNA splicing: nucleotide A;Reference number: A91075; MUID:88004424; PMID:2443348
                                                                                                                                                                                                                                                           C;Accession: T06667
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; Oheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schueller, C. submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15792
A;Accession: T06667
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                                                                                                                                                    argininosuccinate synthase (BC 6.3.4.5) - Arabidopsis thaliana N;Alternate names: protein F617.40 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #sequence_revision 23-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
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A;Residues: 1-181,'P',183-317,'A',319-363 <KRE>
A;Cross-references: EMBL:X05509; NID:g3987; PIDN:CAA29053.1; PID:g3988
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Cross-references: EMBL:AL049657; GSPDB:GN00062; ATSP:F617.40
A;Experimental source: cultivar Columbia; BAC clone F617
C;Genetics: ASP:F617.40
A;Map position: 4
A;Introns: 25/1; 100/1; 146/2; 162/3; 223/3; 285/3; 315/2
C;Superfamily: argininosuccinate synthase
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.4%; Score 71; DB 2; Length 498; 25.3%; Pred. No. 6.7; ive 18; Mismatches 36; Indels
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306 AKIRVKESIDVLEELKILVDYDEKGYLLQI 335
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submitted to the EMBL Data Library, October 1994
A;Reference number: S48478
A;Accession: S48483
A;Molecule type: DNA
A;Residues: 1-363 <ROW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRS1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YIR021w
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Matches 21; Conservative
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A,Genome: nuclear
C,Keywords: mitochondrion
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A; Residues: 1-498 <BEV>
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004801; F:stanscription factor activity; IEA.
GO; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IRR008967; PS3 like_DNA_bnd.
InterPro; IRR008967; ST3 like_DNA_bnd.
Pfam; PF02064; STATalbha; 1.
Pfam; PF02864; STAT_bind; 1.
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Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
       Q14765
Q801y2
Q801y2
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Signal transducer and activator of transcription (Fragment)
Name-STAT3;
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100.0%; Pred. No. 1.3e-46;
ive 0; Mismatches 0; Indels
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF27560; AF73401.1; -.
HSSP; P42227; 1BG1...7... TEA
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DT 05-UUL-2004 (Rel. 44, Last sequence update)

DT 25-UUL-2004 (Rel. 45, Last annotation update)

DT 25-CT-2004 (Rel. 45, Last annotation update)

E Signal transducer and activator of transcription 3.
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                                                                                                                        May 25, 2005, 17:15:30 ; Search time 39.944 Seconds (without alignments) 1230.701 Million cell updates/sec
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                                                                                                                                                                                           US-10-090-185-25
494
1 KKLEELQQKVSYKGDPIVQH......LNYQLKIKVCIDKDSGDVAA
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O13131
O13132
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06dv79
09gvx8
070xx8
072x8
072x8
072x8
09359
06dv46
060v46
060v46
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Q6p6q7
Q8c497
Q9qxk0
Q99k94
Q8c3v4
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P42224
Q68d00
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P40763
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                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                 1612378 seqs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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STA1_HUMAN
Q68D00
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STA3 BOVIN
STA3 HUMAN
STA3 AUGUSE
STA3 RAT
06DV79
009PVX8
0704W5
07ZXX3
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Maximum Match 100%
Listing first 45 summaries
                                                                                             OM protein - protein search, using sw model
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093599
Q6DVF3
Q6GUE7
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Q6P6Q7
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Q9QXK0
Q99K94
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Q90Y17
Q764M5
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013131
013132
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length DB
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Result No. ö

Gaps

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                   1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 60
                                                                                                                                                                                                                                                                                                                                   Phosphotyrosine (by JAK) (By similarity). Phosphoserine (By similarity). 9CEB147C73E83274 CRC64;
                                                                                                                                                                                                                                                                                                  PROSITE; PS50001; SH2; 1. Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,
             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STA3 HUMAN STANDARD; PRT; 770 AA.
P40763; 014916; Q9BW54;
01-F8E-1995 (Rel. 31, Created)
05-JUL-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase
                                                                                                                                                                                                                                                                                                                                                                       Length 770;
                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 494; DB 1;
100.0%; Pred. No. 7.7e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                         EMBL; AJ620655; CAF06182.1; -.
                                                                                                                                                                                                                                                                                                                                                      770 AA; 87974 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 response factor).
Name=STAT3; Synonyms=APRF;
                                                                                                                                                                                                                                                                                                                    Pranscription regulation.
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nes 96; Conservative
                                                                                                                                                                                                                                                                                                                                              727
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       taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                           NCBI_TaxID=9913;
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MOD_RES
SEQUENCE
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TISSUEEKidney, and Pancreas;

TISSUEEKidney, and Pancreas;

MEDINRE_2528825; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse J.H., Derge J.G.,

Altachul S.F., Zeeberg B., Buerow K.H., Schemen.C.M., Schuler G.D.,

Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altachul S.F., Zeeberg B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunzratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B., Monerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giraud S., Blenvenn F., Avril S., Gascan H., Heery D.M., Coqueret O., "Functional interaction of STAT3 transcription factor with the coactivator NcoA/SRC1a.";
J. Biol. Chem. 277:80104-8011(2002)
- FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6) responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acute-phase protein genes.
--- PATHWAY: Involved in the gp130-mediated signaling pathway.
--- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOA1.
--- SUBCELLUIAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.
Yoshida K., Sudo T., Naruto M., Kishimoto T.; "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related transcription factor involved in the gp130-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOPORM DEL-701), AND VARIANT ILE-143.
Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
Rajkumar N., Yi Q., Nickerson D.A.;
"SeattleSNPs. NHLBI Hi66682 program for genomic applications, UW-
FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
"Requirement of serine phosphorylation for formation of STAT-promoter
                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-98296260; PubMed-9630560; DOI=10.1016/S0378-1119(98)00185-1;
Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenti O.;
"Highly conserved amino-acid sequence between murine STAT3 and a revised human STAT3 sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 213:119-124(1998)
                                                                                                                                                                                                      Cell 77:63-71(1994).
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STA3_MOUSE
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                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@1sb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005602; F:hematopoietin/interferon-class (D200-domain. .; TAS.
GO; GO:0005062; F:hematopoietin/interferon-class (D200-domain. .; TAS.
GO; GO:0007209; P:call motility; TAS.
GO; GO:0007229; P:JAK-STAT cascade; TAS.
GO; GO:0007229; P:JAK-STAT cascade; TAS.
GO; GO:0007329; P:INEUTOGENESIS; TAS.
GO; GO:0007145; P:INEUTOGENESIS; TAS.
InterPro; IPRO009807; PS3_like_DNA_bnd.
InterPro; IPRO009807; PS3_like_DNA_bnd.
InterPro; IPRO009807; PS3_like_DNA_bnd.
                          ISOIG=P40763-2; Sequence=VSP 010474;
-!- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal muscle, Kidney and pancreas.
-!- FTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, LIP, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity.
-!- SIMILARITY: Balongs to the transcription factor STAT family.
-!- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphotyrosine (by JAK) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Activator; Alternative splicing; DNA-binding; Nuclear protein;
Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 494; DB 1; Length 770; 100.0%; Pred. No. 7.7e-46; cive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F -> Y (in Ref. 1).
V -> L (in Ref. 1).
T -> A (in Ref. 1).
; 6C00632211C8012D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q -> K (in dbSNP:1803125)
/FTId=VAR_018683.
M -> I.
/FTId=VAR_018679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (in Ref. 1).
IsoId=P40763-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VSP
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                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC014482; AAH14482.1; -. EMBL; AF029311; AAB84254.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PP00017; SH2; 1.
Pfam; PP01017; STAT alpha; 1.
Pfam; PP02864; STAT bind; 1.
Pfam; PP02865; STAT int; 1.
PROSITE; PS50001; SH2; 1.
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Best Local Similarity 100.0
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSFAC; T01493; -. Genew; HGNC:11364; STAT3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                701
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667
730
770 AA;
              Name=Del-701
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282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPM4PDRPLVIKT 341
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"Acute phase response factor and additional members of the interferon-
stimulated gene factor 3 family integrate diverse signals from
cytokines, interferons, and growth factors.";
J. Biol. Chem. 269:24391-24395(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALBAC; TISSUE=Liver;
MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
Yoshida K., Sudo T., Naruto M., Kishimoto T.;
"Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
related transcription factor involved in the gpl30-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Thymus;
MEDLINE=94188718; PubMed=8140422;
Zhong Z., Wen Z., Darnell J.E. Jr.;
"Stat3: a STAT family member activated by tyrosine phosphorylation in response to epidermal growth factor and interleukin-6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM STAT3B).
STRAIN=BALB/c, and CS7BL/6; TISSUB=Liver;
MEDLINE=96016116; PubMed=7568080;
Schaefer T.S., Sanders L.K., Nathans D.;
"Cooperative transcriptional activity of Jun and Stat3 beta, a short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J, and NOD/LtJ;
Davoddi-Semiromi A., She J.-K.;
A mutant Stat5b with weaker DNA binding defines a key defective pathway in non-obese diabetic (NOD) mice.";
                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase response factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=11161808; DOI=10.1006/geno.2000.6433;
Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T.,
Dewar K., Hennighausen L.;
                                                                                   GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                       96
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                                                         GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA
                                                                                                                                                                                                                           01-007-1995 (Rel. 32, Created)
01-00T-1996 (Rel. 34, Last sequence update)
25-00T-2004 (Rel. 45, Last annotation update)
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MEDLINE-95014185; PubMed-7523373;
                                                                                                                                                                                                                                                                                                                                Name=Stat3; Synonyms=Aprf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               zebrafish to mouse.";
Genomics 71:150-155(2001).
                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 264:95-98(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell 77:63-71(1994).
                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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SEQUENCE FROM N.A. (ISOFORM STAT3A).

SEQUENCE FROM N.A. (ISOFORM STAT3A).

STRAIN=FVBN, TISSUE=Mammary gland;

MEDINE=2238825; PubMed=1247932; DoI=10.1073/pnas.242603899;

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schnefer C.F., Bahat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tonahlow R.C., Caraninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Makek J.A., Gunbaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesbey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka W.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka W.,

Butterfield Y.S.N., Marshan J.W., Marra M.A.,

Butterfield Y.S.N., Marshan M.A.,

Butterfield W. Madan A., Sohein J.B., Jones B.J.M., Marra M.A.,

Butterfield Y.S.N., Marshan J.W., Marra M.A.,

Butterfield Y.S.N., Marshan J.B., Marra M.A.,

Butterfield
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-I- FUNCTION: Transcription factor that binds to the interleukin-6

-I- FUNCTION: Transcription factor that binds to the interleukin-6

(IL-6)-responsive elements identified in the promoters of various acute-phase protein genes. STAT3B interacts with the N-terminal part of JUN to activate such promoters in a cooperative way.

-I- PATHWAY: Involved in the gp130-mediated signaling pathway.

-I- SUBCELLULAR is a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).

-I- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.

-I- ALTERNATIVE PRODUCTS:

-I- ALTERNATIV
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PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS,
PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS,
MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
Wen Z., Zhong Z., Darnell J.E. Jr.;
"Maximal accivation of transcription by Statl and Stat3 requires both tyrosine and serine phosphorylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Dol-701;
Squence=VSP 010475;
Isole=P42127-3; Sequence=VSP 010475;
TISSUE SPECIFICITY: STAT3A is Seen in the liver, spleen, and kidney. STAT3B is also detected in the liver, although in a much less abundant manner.

PTW: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, ILF, CSF-1, ESF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 in mondiners and maximal transcriptional activity (By similarity). SIMILARITY: Belongs to the transcription factor STAT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
MEDLINES-98334771; PubMed-9671289; DOI=10.1038/28101;
Becker S., Groner B., Mueller C.W.;
"Three-dimensional structure of the Stat3beta homodimer bound to
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Name=Stat3B;
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FDMDLTSECATSPM -> FIDAVWK (in isoform
Stat3B).
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       EMBL; 129278; AAA19422.1; -..

REMBL; 106922; AAA19422.1; -..

REMBL; 106922; AAA19422.1; -..

REMBL; 108709; AAC52612.1; -..

REMBL; AR246978; AAA159017.1; -..

REMBL; AX299489; AAA075418.1; -..

ROG GO:000589; Colouses in Dinding; IDA.

GO; GO:000589; Colouses in Dinding; IDA.

GO; GO:0007259; Pirkenscriptional activator activity; IDA.

GO; GO:0007259; Pirkenscriptional activator activity; IDA.

GO; GO:0007259; Pirkenscriptional activator in Day.

GO; GO:0007259; Pirkenscriptional activator in Day.

RITHERPO; IPR000980; SHZ.

RITHERPO; IPR000980; SHZ.

RITHERPO; PR00017; SHZ; 1.

REAM; PR0017; SHZ; 1.

REAM; REMBL; REMBL; REMARENCE ACTIVATOR; ACUTE phase; Alternative splicing; DIA-CATIVATOR; ACTIVATOR; ACTI
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/FTId=VSP_010475.
S->A: Decreased transcriptional
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S -> T (in Ref. 2 and 4).
M -> I (in Ref. 1).
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STA3 RAT

RESULT 5

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282 KKLEELQQKVSYKGDPIVQHRPMLEERIVDLFRNIMKSAFVVERQPCMPMHPDRPLVIKT 341
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Chounger, E. C., and C. C., and C., and C. C., and C. C., and C., and C., and C., and C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal transducer and activator of transcription 3. Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 771;
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Last annotation update)
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99.0%; Pred. No. 2.1e-45;
iive 0; Mismatches 1;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
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Les 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Transcription factors Stat3 and Stat5b are present in rat liver nuclei late in an acute phase response and bind interleukin-6 response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphotyrosine (by JAK) (By similarity). Phosphoserine (By similarity). D74A0C76954754ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 270:29998-30006(1995).
-!- FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998;
Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
770 AA
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InterPro; IPR000980; SH2.
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Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
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Matches 95; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Stat3;
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MOD_RES
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Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;

Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;

Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

Shafish Ad20661; CaF60188.1; -.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0004871; F:signal transducer activity; IEA.

R GO; GO:0003700; F:transcription factor activity; IEA.

R GO; GO:000615; P:signal transduction; IEA.

R GO; GO:000615; P:signal transduction; IEA.

R GO; GO:000615; P:signal transduction; IEA.

R InterPro; IPR001217; STAT.

R InterPro; IPR001217; STAT.

R Pfan; PF01017; STAT. alpha; 1.

R Pfan; PF02864; STAT. bind; 1.
                                                                                            R GO; GO:0005634; C:nucleus; IEA.
R GO; GO:0005634; C:nucleus; IEA.
R GO; GO:0007242; F:signal transcurent activity; IEA.
R GO; GO:0007242; P:intracellular signaling cascade; IEA.
R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
R InterPro; IPR00980; SH2.
R InterPro; IPR00980; SH2.
R Pfam; PF00117; SH3.
R Pfam; PF00117; SH3.
R Pfam; PF00117; SH3.
R Pfam; PF00155; STAT_alpha; 1.
R Pfam; PF02864; STAT_alpha; 1.
R Pfam; PF02864; STAT_int; 1.
R Pfam; PF02864; STAT_int; 1.
R Pfam; PF02864; STAT_int; 1.
R Pfam; PF02864; SH3T_int; 1.
R Pfam; PF02864; SH3T_int; 1.
R Pfam; PF02864; SH3T_int; 1.
R PRAM; SM00252; SH3T_int; 1.
R PRAM; SM00252; SH3T_int; 1.
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Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T., Asashima M., Yokota T.; "Activation of Stat3 by cytokine receptor gpl30 ventralizes Xenopus embryos independent of BMP-4."; Dev. Bol. 216:481-490(1999).

EMBL; AB017701; BAA86061.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Mammary gland;
Molenaar A., Wheeler T.T., McCracken J.Y., Seyfert H.M.;
The STAT3-encoding gene resides within the 40 kbp gap between the
STATSA- and STATSH-encoding gene in cattle.";
Anim. Genet. 31:333-334(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name-stat3;
Boss taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Signal transducer and activator of transcription 3 (Fragment).
                                                                                                                                                                                                                                                                                                                  99.0%; Score 489; DB 2; Length 769; 99.0%; Pred. No. 2.8e-45; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           342 GVQFTNKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                              61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 AA.
                                                                                                                                                                                                                                                                                                                                  Local Similarity 99.0
nes 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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MEDINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raha S.S., Morley K.C., Hale S., Garcia A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M. Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
A Hilalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
A Hilalon B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Hakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Marra M.A.,
A Jones S.J., Marra M.A.,
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                                                                                                                                                                                                            9
                                                                                                                                                                                                         1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                                                                                                                                                                                                                                            16 KKLEGLQQKVSYKGDPIVQHRPMLEBRIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                   .
0
                                                                                   Score 487; DB 2; Length 161; Pred. No. 7.7e-46;
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                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUB=Embryo;
Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO447171; AAH44717.1;
HSSP; P42227; 1BG1.
161
18342 MW; 5DCEE8F2C3A48191 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005634; C:nucleus; IEA.
GO: GO:0004871; F:signal transducer activity; IEA.
GO: GO:0003700; F:transcription factor activity; IEA.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                               98.6%; Score 7.7e-99.0%; Pred. No. 7.7e--99.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. Dyn. 225:384-391(2002)
                                                                                                                                                      95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae, Xenopus.
   161 1
161 AA;
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                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stat3-A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=stat3-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              initiative."
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Q6NV46
                                                                                                                                                                                  Matches
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ID O6
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                                                                                                                                                                                                                                                                                                                                                                           STRAIN=AB; TISSUB-Whole body;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Astaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ralauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEvan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Malek J.D., N., Sodergren E.J., Lu X., Gibbs R.A.,

Richards M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radsiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.,

"Grimera D. K., Schilka U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Grimera D. K., Schilka U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                   1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNIMKSAFVVERQPCMPMHPDRPLVIKT
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
NCBI_TaxID=7955,
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000967; PS3_like_DNA_bnd.
InterPro; IPR001217; STAT.
InterPro; IPR001217; STAT.
FEan; PP01017; STAT.
Fean; PP01017; STAT_alpha; 1.
FEan; PP0264; STAT_blind; 1.
Fean; PP0265; STAT_blind; 1.
Fean; PP0265; STAT_blind; 1.
Fean; PF0265; STAT_blind; 1.
SWART; SM00252; SHZ; 1.
SROWENCE 766 AA; 87599 MW; 31018A3321CCEB9C CRC64;
                                                                                                                                                                                                           ;
                                                                                                                                                                             96.2%; Score 475; DB 2; Length 766; 95.8%; Pred. No. 9.7e-44; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO4527; AAH45276.1;
HSSP; P42227; 1BG1.
ZFIN; ZDB-GENE-980526-68; stat3.
                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                       414 AA.
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                                                                                                                                                           Query Match
Best Local Similarity >-.
Local 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stat3 protein.
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Q7ZTS5;
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MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE=22388257; PubMed E.A., Grouse L.H., Derge J.G.,

MAISTON COlling F.S., Magner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MEDINES M. M., Machan T.B., Toshiyuki S., Carninci P., Prange C.,

METARA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Nones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human

and mouse CDNA sequences.";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008967; FS3 like_DNA_bnd.
Ftam; PF01017; STAT_alpha; 1.
Ftam; PF02864; STAT_alpha; 1.
Ftam; PF02864; STAT_bind; 1.
Ftam; PF02865; STAT_init; 1.
SEQUENCE 414 AA; 48253 MW; OFFD1B509B7526BD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 414;
                                                                                                                                                                                                                                                                                                                                                                                             96.0%; Score 474; DB 2; Length 41 93.8%; Pred. No. 6.2e-44; ive 5; Mismatches 1; Indels
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Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases
EMBL; EDGENE-980526-68; stat3.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 GVQFTTKVRLLVKFPELNYQLKIKVCIDKESGDVAA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 93.8 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyprinidae; Dani
NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=stat3;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
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SEQUENCE
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                 RESULT 13
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                                      O6DVF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                        1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
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                                                                                                                                                                                                                                                                   Gaps
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Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thesis (1998), University of Melbourne, Australia.

EMBL, AJ005693; CAA06677.1; -.

EMBL, AJ005693; CAA06677.1; -.

EFIN, ZDB-GENE-980526-68; stat3.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:000471; F:signal transducer activity; IEA.

GO; GO:000740; F:transcription factor activity; IEA.

GO; GO:000742; P:intracellular signaling cascade; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000980; SHI2.
transcription, DNA-dependent; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                      Length 786;
                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         806 AA; 92151 MW; 74BC4EA401C3C942 CRC64;
                                                                                                                                                                                  90039 MW; FC7371D0B0E5447E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343 GVQFTTKVRLLVKFPELNYQLKIKVCIDKESGDVAA 378
                                                                                                                                                                                                                                                                                                                                                                                                               343 GVQFTTKVRLLVKFPELNYQLKIKVCIDKESGDVAA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
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                                                                                                                                                                                                                        96.0%; Score 474; DB 2;
93.8%; Pred. No. 1.3e-43;
cive 5; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       806 AA.
                 InterPro; IPR008967; P53_like_DNA_bnd
InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
P:regulation of
                                                                           Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 786 AA; 90039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2004 (TrEMBLrel. 26, Transcrive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PP02865; STAT_int; 1
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 806 AA; 92151 MM
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                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription factor.
                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
GO; GO:0006355;
                                                                                                                                                                                                                                                                 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=stat3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oates A.C.;
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283 KKLEELQQKVSYKGDPIIQHRPALEEKIVDLFRNLAKSAFVVERQPCMPMHPDRPLVIKT 342
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25-OCT-2004 (TrEWBLrel. 28, Created)
25-OCT-2004 (TrEWBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Signal transducer and activation of transcription factor 3.
Oryzias latipes (Medaka fish) (Japanese ricefish).
Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Buteleostomi; Actinopterygii; Neoterygii; Teleostei; Euteleostei; Meotleostei; Acanthomorpha; Acanthoterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TTEMBLrel. 27, Last sequence update)
05-JUL-2004 (TTEMBLrel. 27, Last annotation update)
Signal transducer and activator of transcription 3 isoform 1.
Oryzias latipse (Medata fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intraccllular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008967; P53_like_DNA_bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu R., Hong Y.;
Liu R., Dong Y.;
Liu R., Dong Y.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AX639947, AAT64912.1;
GO; GO:00056534; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007300; F:transcription factor activity; IEA.
GO; GO:0007320; F:transcription factor activity; IEA.
GO; GO:0007321; P:negulation of transcription, DNA-dependent; IEA.
InterPro; IPR000980; FS1.
InterPro; IPR000317; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.5%; Score 472; DB 2; Length 765; 93.8%; Pred. No. 2.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu R., Hong Y.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY641434; AAT46364.1; -..
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Pfam; PP01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PP02865; STAT int; 1.
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Best Local Similarity
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                                                                                                                                                                                                                        1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 60
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                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P4227; 1BG1.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0004871; F:signal transducer activity; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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0
                                                                                                                                                        Length 785;
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                                                                                                                                                    95.5%; Score 472; DB 2; Length 78 93.8%; Pred. No. 2.2e-43; vative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF307106; AAL09415.1; -.
                                                                                                                    89643 MW; 81F231BDE27DE938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SH2; 1.
; 87411 MW; E661FFE18BEFD8BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q90Y16;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                              343 GVQFTNKVRLLVKFPELNYQLKIKVCIDKESGDVAA 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                     764 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodon fluviatilis (Puffer fish)
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                              Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 785 AA; 89643 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PP00017; SH2; I.
Pfam; PP01017; STAT_alpha; I.
Pfam; PP02864; STAT_bind; I.
Pfam; PP02865; STAT_int; I.
SWART; SM00252; SH2; I.
                                                                                                                                                                      Local Similarity 93.8 see 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.7<sup>3</sup>
Matches 88; Conservative
 InterPro; IPR000980; SH2
                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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PROSITE; PS50001;
SEQUENCE 764 AA;
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Search completed: May 25, 2005, 17:43:42 Job time : 40.9444 secs

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Mouse Sta Mouse Sta Mouse Sta Mouse Sta Mouse Sta Rat STAT-Human tru Human exp Truncated

Aay72851 Aay72847 Aay72855 Aay72855 Aay72855 Aay72862 Aay72862 Aay72862 Aay72865 Aay72849 Aay72844 Aay72844 Aay72844 Aay72844 Aay72844 Aay72844 Aay72879 Abu04748 Aaw62995 Abaw62995 Abaw62995 Abaw62995 Abaw62995 Abaw62995

Mouse Mouse

Human sig Human Sta

Human Human

Human Human

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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/note= "Wild type Val substituted with Ala corresponds to 151 position of Stat-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild type Leu substituted with Ala; corresponds
to 148 position of Stat-3 protein"
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild type Lys substituted with Ala corresponds
348 position of Stat-3 protein"
221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild type Arg substituted with Ala corresponds 350 position of Stat-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis; therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213. 229
/note= "Stat1-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse Stat3 mutant (L148A, V151A, T346A, K348A, R350A) protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild type Thr substituted with Ala 346 position of Stat-3 protein" Misc-difference 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                         AAY72851
AAY72847
AAY72854
AAY72855
AAY72852
AAY72862
AAY72892
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AAY72894
AAW62995
AAW0170
AAW617070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . AAY72860 standard; protein; 229 AA
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/note= '
                                           Misc-difference
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Aay72850 Mouse
                                                                                                                                                                                                                                                             1 NHPTAAVVTEKQQMLEQHLQ......IKTGVQFATAVALLVKFPEL 229
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                               2105692 seqs, 386760381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 OM protein - protein search, using sw model
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AAY72841
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AAE22055
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ADD44738
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AAR82993
AAB19964
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Gapop 10.0 , Gapext 0.5
                                                                                                                                         May 25, 2005, 17:14:45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      geneseqp20028;*
geneseqp2003as;*
geneseqp2003bs;*
geneseqp20048;*
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seq length: 200000000
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1169
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61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                                                                                                                                                                                                                                                                                                                                                                   The present sequence is mouse Stat3 protein fragment containing 130-358 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of sysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                              Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 VELFRNIAKSAFVVERQPCMPMFPDRPLVIKTGVQFTTKVRLIVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse Stat3 protein fragment #4 (107-358 amino acids).
                                                                                                                                                                         Darnell JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1155; DB 4;
Pred. No. 4.4e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.9%; Scor. 98.7%; Pred. No. 4... 98.7%; O; Mismatches
                                                                                                                                                                         Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                 Claim 65; Page 76-77; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY72846 standard; protein; 252
                                       30-AUG-2000; 2000WO-US023822.
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Matches 226; Conservative
                                                                                                                                UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                         Zhang X, Horvath C,
                                                                                                                                                                                                                   WPI; 2001-226705/23.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 229 AA;
                                                                                    31-AUG-1999;
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08-MAR-2001
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Region
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                                                                                                                                                                                                              The present sequence is mouse Stat3 mutant protein fragment containing replacing of Stat3 protein. This mutant is obtained by replacing Leu 148 with Ala, val 151 with Ala, Thr 346 with Ala, Lys 348 with Ala and Arg 350 with Ala in the Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comperises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDMQDLN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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/note= "Stat3-c-Jun interaction region 1; corresponds 130-154 position of Stat3 protein"
213. .229
/note= "Stat3-c-Jun interaction region 2; corresponds 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse, Stat3 protein, transcription factor; c-Jun, gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                         Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1160; DB 4; Length 229;
Pred. No. 1.5e-98;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse Stat3 protein fragment #8 (130-358 amino acids).
                      Darnell JE;
                    Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY72850 standard; protein; 229
                                                                                                                                                                         Example 4; Page; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 99.1
Matches 227; Conservative
                    Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200116605-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                      Zhang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy.
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Region
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RESULT 2 AAY72850

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Length 229; 3; Indels 9

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08-MAR-2001

Zhang X,

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GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is mouse Stat3 protein fragment containing 107-377 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a renacription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of typroliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, bund binding domain, linker domain, SH2 domain and transactivation domain
                                           interaction region 1; corresponds Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLBERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.8%; Score 1155; DB 4; Length 271; 98.7%; Pred. No. 5.5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VELPRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL
                                      /note= "Stat3-c-Jun interaction region 1; 130-154 position of Stat3 protein" 252. 252 /note= "Stat3-c-Jun interaction region 2; 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                           Darnell JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 65; Page 67-68; 86pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR72082 standard; protein; 770 AA
                                                                                                                                                                                                                                                  30-AUG-2000; 2000WO-US023822.
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                                                                                                                                                                                                                                                                                                                                                                           Zhang X, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-226705/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Stat3 (19sf6)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 271 AA;
                                                                                                                                                                    WO200116605-A2
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27-SEP-1995
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is mouse Stat3 protein fragment containing 107-358 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of Stat protein comprises the N-terminal domain, colled-coil domain, bind binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
  corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACIGGPPNICLDRLENWITSLAESOLOTROOIKKLEELQQKVSYKGDPIVQHRPMLEERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                        Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1155; DB 4; Length 252;
Pred. No. 5e-98;
0; Mismatches 3; Indels (
/note= "Stat3-c-Jun interaction region 2;
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse Stat3 protein fragment #2 (107-377 amino acids)
                                                                                                                                                                                                                                                                        Darnell JE;
                                                                                                                                                                                                                                                                        Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 65; Page 73; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY72841 standard; protein; 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.88;
98.78;
                                                                                                                                              30-AUG-2000; 2000WO-US023822
                                                                                                                                                                                     99US-00387418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 98.7
Matches 226; Conservative
                                                                                                                                                                                                                              (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                        Horvath C,
                                                                                                                                                                                                                                                                                                                 WPI; 2001-226705/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 252 AA;
                                                              WO200116605-A2
                                                                                                                                                                                     31-AUG-1999;
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121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New STAT protein DNA-binding domain peptide(s) - useful for diagnosing, preventing or treating cellular dysfunction, e.g. oncogenesis, inflammation, parasitic disease or autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse signal transducer and activator of transcription (STAT) protein STAT4 (AAM01176) serves a dual purpose, i.e. signal transduction from ligand-activated receptor kinase complexes followed by nuclear translocation and DNA binding to activate transcription. Recombinant STAT4 can be obtd. using cDNA clone 19sf6 (AAT31278) obtd. from splenic/thymic cells. STAT4 includes a DNA-binding domain (see also AAW03167) capable of both receptor recognition and message delivery vi DNA binding in a receptor-ligand specific manner. STAT proteins and the DNA binding domains (see also AAW03165-75) are useful for screening antagonists used to inhibit STAT-mediated signal transduction and activation of transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STAT; STAT4; signal transducer and activator of transcription; DNA binding protein; ligand; receptor; oncogenesis; inflammation; autoimmune disease; antagonist; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.8%; Score 1155; DB 2; Length 770; 98.7%; Pred. No. 2.2e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFATAVALLVKFPEL
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                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 87-90; 138pp; English.
                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                      Horvath
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Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                (UYRQ ) UNIV ROCKEFELLER
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                                                                                                                                                                                                                                                                                                                                                                                                      Wen Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT31280
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                                                                                                                                                                                                               WO9620954-A2
                                                                                                                                                                                                                                                                                         28-DEC-1995;
                                                                                                                                                                                                                                                                                                                             06-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                    Darnell JE,
                                                                                                                                                                                                                                                     11-JUL-1996.
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Best Local S
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                                                                                                                   Key
Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in AAQ89338) was isolated that encoded a 91 Kna protein (AAR72080) (Stat1) that was responsive to interferon-gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AAQ89339-40) were cloned in plasmids 13sfl and 19sf6 and encoded proteins termed Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 NHPTAAVVTEKQOMLEQHLQDVRKRVQDLEQXMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249
Signal transducer and activator of transcription; STAT; 19sf6; Stat3; receptor recognition factor; transcription factor; cellular debilitation; derangement; dysfunction; interferon-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1155; DB 2; Length 770;
Pred. No. 2.2e-97;
0; Mismatches 3; Indels (
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                                                                                                                                                                                                                                                                                                                                                                    Wen Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 107-110; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                    Shuai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW03176 standard; protein; 770 AA
                                                                                                                                                                                                                               93US-00126588.
93US-00126595.
94US-00212184.
94US-00212185.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 98.7
Les 226; Conservative
                                                                                                                                                                                                                                                                                                                               (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-139598/18.
                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ89340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 770 AA;
                                                                                                                                                                                                                               24-SEP-1993;
24-SEP-1993;
11-MAR-1994;
11-MAR-1994;
                                                                                                                 WO9508629-A1
                                                                                                                                                                                           26-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                    Darnell JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-1996
                                                                                                                                                       30-MAR-1995
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Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                        Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids).
                                                                      AAY72862 standard; protein; 229 AA
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                                                                                                                                                                                                                                                 therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang X, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-226705/23
                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                        31-MAY-2001
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                                                                                                         AAY72862;
                                                                                                                                                                                                                                                                                                                    Key
Region
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                                    RESULT, 8
                                                      AAY72862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is mouse Stat3 mutant (V151A) protein fragment containing 130-358 amino acids of Stat3 protein. This mutant is obtained by replacing val 151 with Ala in Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., callular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A
                                                                                                                                                                                                                                                                                                                    ដ
                                                                                                                                                                                                         /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"
                                                             Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis; therapy; mutant; mutein.
                                                                                                                                                                                                                                                            'note= "Wild type Val substituted with Ala corresponds
                                                                                                                                                                                                                                                                                                  213. .229
/note= "Stat3-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying an agent for use in modulating the interaction between
                                Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1151; DB 4; Length 229;
Pred. No. 1e-97;
0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Darnell JE;
                                                                                                                                                                                                                                                                                151 position of Stat-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription factor c-Jun and a Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang X, Horvath C, Wrzeszcynska MH,
                                                                                                                                                                        location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 66; Page 86; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00387418.
                                                                                                                                                                                                                                                                                                                                                                                                                                        30-AUG-2000; 2000WO-US023822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.5%;
(first entry)
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Best Local Similarity 98.3°
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-226705/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 229 AA;
                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                   WO200116605-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-AUG-1999;
                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-2001
                                                                                                                                                                        Key
Region
                                                                                                                                                                                                                                                                                                  Region
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213. .229 /note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"

Darnell JE;

Wrzeszcynska MH,

99US-00387418.

/note= "Wild type Leu substituted with Ala; corresponds to 148 position of Stat-3 protein"

/note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"

Location/Qualifiers

(first entry)

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                                                                                                                                                                                               containing 130-158 amino acids of Stat3 protein. This mutant is obtained by replacing Leu 148 with Ala in Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                          The present sequence is mouse Stat3 mutant (L148A) protein fragment
Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.4%; Score 1150; DB 4; 98.3%; Pred. No. 1.3e-97; ive 0; Mismatches 4;
                                                                                                   Claim 66; Page 85; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.3
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 229 AA;
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NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN NHPTAAVVTEKQQMLEQHLQDARKKVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

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ACIGGPPNICLDRLENWITSLAESQLOTRQOIKKLEELQQKVSYKGDFIVQHRPMLEERI

VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 229 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229

ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI

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ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modulating anglogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                               Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; angiggenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; sjogren's syndrome; multiple sclerosis; Addison's disease; spilepsy, polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion; Statbeta.
                                                                     VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
713. .714
/note= "Encoded by ACA CCA TTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dalton W;
                                                                                                                                                      AAE22055 standard; protein; 720 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jove R,
                                                                                                                                                                                                              (first entry)
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(UYSF-) UNIV SOUTH FLORIDA
                                                                                                                                                                                                                                       Human Stat3beta protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-362218/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu H, Pardoll D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD35066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                             25-JUL-2002
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                                                                                                                                                                                  AAE22055;
121
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with necvascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus cryptematosus, multiple sclerosis, inaulin dependent diabetes mellitus, sjoyramus, scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, julten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune confirs and dense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and carrinomas eg., bladder darscinoma, colon carrinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The criptonic control of the present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 AÇIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse ischaemic condition related protein sequence SEQ ID NO:398.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease.
                                                                                                                                                                                                                                                                                                                                                                    Score 1144; DB 5; Length 720;
Pred. No. 2e-96;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB57164 standard; protein; 769 AA
                                                                                                                                                                                                                                                                                                                                                                  97.98;
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                                                                                                                                                                                                                                                                                                                                                                                                      Matches 224; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-034733/04.
N-PSDB; ABI99454.
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                Stat3beta protein
                                                                                                                                                                                                                                                                                                                                Sequence 720 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-NOV-2001
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Best Local 8
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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, trauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphysia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy

Disclosure; Page 87-89; 94pp; English.

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conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic condition-improving drugs or therapeutics for ischaemic condition related sequence, which are used in the exemplification of the present invention
determining the expression profile of a gene group comprising these
                                                                                                                                         present invention describes a method for examining ischaemic
                                                                                 Claim 2; Page 1084-1087; 2690pp; English.
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Sequence 769 AA;

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130 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDPDFNYKTLKSOGDMODLN 189
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                                                                                                                                                    ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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                                                                  1 NHPTAAVVTEKOOMLEQHLODVRKRVODLEQKMKVVENLODDFDFNYKTLKSQGDMODLN
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                                Gaps
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                                                                                                                                                                                                                                                                    VELFRNIMKSAFVVEROPCMPMHPDRPLVIKTGVOFATAVALLVKFPEL 229
                                                                                                                                                                                                                                                                                     VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
Score 1144; DB 5; Length 769; Pred. No. 2.2e-96;
                                  4; Indels
                                  1; Mismatches
 97.9%;
Query Match 97.9
Best Local Similarity 97.8
Matches 224; Conservative
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AAE22054 standard; protein; 769 AA. 25-JUL-2002 (first entry) Human Stat3 protein. AAE22054; RESULT

immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; hypoxlycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetee mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion. Human; signal transducer and activator of transcription 3; ischaemia;

Homo sapiens

WO200220032-A1.

14-MAR-2002

10-SEP-2001; 2001WO-US028254.

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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that condulate the activity of signal transducer and activator of transcription of Stat13). Modulating angiogenesis is useful for treating or preventing thypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia in the lower extremities, infarction, inflammation, trauma, vascular occlusion, prematal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chitogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus crythematosus, multiple sclerosis, insulin dependent diabetes mellitus, contenting a syndrome, scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, permicious canemia, autoimmune thyroditis, idiopathic Addison's disease, victuating arthritis, discommune neutropenia myasthenia gravis, disease, rheumatoid arthritis, discomia neutropenia, myasthenia gravis, disease, theumatoid arthritis, cirrhosis, pemphygus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating charging and province of the sease of the sease. The method is useful in preventing or treating specific proliferative and oncogenic disease, premicionic, proliferating and propertions.
                                                                                                                                                                                                                                                                                             Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical leama, lesions and wounds. The method is also used in gene therapy. The present sequence is human Stat3
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 83-85; 94pp; English.
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                                                                                                                                                              Dalton
                         08-SEP-2000; 2000US-0231212P
                                                                                                                                                              Jove R,
                                                                            (UYJO ) UNIV JOHNS HOPKINS. (UYSF-) UNIV SOUTH FLORIDA.
                                                                                                                                                                                                                    WPI; 2002-362218/39.
                                                                                                                                                                                                                                                                                                                                                                                     transcription 3.
                                                                                                                                                              Yu H, Pardoll D,
                                                                                                                                                                                                                                                N-PSDB; AAD35065
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Sequence 769 AA;

Gaps ö 97.9%; Score 1144; DB 5; Length 769; 97.8%; Pred. No. 2.2e-96; 1. Mismatches 4; Indels Best Local Similarity 97.8 Matches 224; Conservative Query Match

1 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFDFNYKTLKSOGDMODLN

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189 130 NHPTAAVVIEKQOMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLM GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI GNNQSVTRQXMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 61 190 셤 셤 8

250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPWLEERI 309 VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358 VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 181

ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI

121

δ 셤 8 용 RESULT 12 AAE22056 H

310

AAE22056 standard; protein; 769

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Sequence 769 AA;

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AAE22056;
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25-JUL-2002 (first entry)

Human protein related to angiogenesis regulation.

Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stard3; coronary atheroselerosis; wascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; drave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.

Homo sapiens.

WO200220032-A1.

14-MAR-2002.

10-SEP-2001; 2001WO-US028254

08-SEP-2000; 2000US-0231212P

o che 2000, 20000 021212

(UYJO) UNIV JOHNS HOPKINS. (UYSF-) UNIV SOUTH FLORIDA.

Yu H, Pardoll D, Jove R, Dalton W;

WPI; 2002-362218/39.

Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator of transcription 3.

Disclosure; Page 83-85; 94pp; English.

The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing thypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, tissue ischaemia or postructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, circonic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, circonic obstructing a symptom of an autoimmune response is useful for with neovascularisation. Suppressing an immune response is useful for with neovascularisation of an autoimmune disease such as systemic lupus erythematosus, multiple sclerosis, insulin dependent diabetes mellitus, sjogren's syndrome, sclerosis, insulin dependent diabetes mellitus, sjogren's syndrome, sclerosis, insulin dependent diabetes mellitus, sjogren's syndrome, sclerosis, primary bilary cirrhosis, permicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, or clidopathic thromborytopenia purpura, Grave's disease, connective tissue disease, primary bilary cirrhosis, autoimmune chyroiditis, idiopathic Addison's disease, is a dependent disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcommas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, chypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The prevent sequence is human expected in gene therapy.

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                                                                                               130 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN 189
                                                                                                                                                                                                  121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                     250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New acute phase response factor - for developing inhibitory agents for treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse, acute phase response factor; transcription factor; interleukin-6; signal transmission; liver; antibody; antisense; ribozyme; antiinflammatory; antitumor; hypotensive; therapy.
                                                                                                                                                    GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
                                                                1 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSQGDMQDLN
                                                                                                                                   GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                                                                 181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 229
                                                                                                                                                                                                                                                                                  VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
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 Length 769;
                                   4; Indels
 Score 1144; DB 5;
Pred. No. 2.2e-96;
1; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                  AAR82995 standard; protein; 770 AA.
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97.9%;
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Query Match
Best Local Similarity 97.8
Matches 224; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-346089/45.
N-PSDB; AAT05619.
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                                                                                                                                                                                                                                                                                                                                                                                                            Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6; intracellular transcription factor; interleukin-6; medicament; variant; pharmaceutical; autoimmune disease; inflammatory; human.
                                                 1 NHPTAAVVTEKQOMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                    GNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
                                                                                                                     GNNQSVTRQKWQQLEQMLTALDQWRRSIVSELAGLLSAMBYVQXTLTDEELADWKRRQQI
                                                                                                                                                       121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                          Gaps
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                                                                                                                                                                                                             VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 229
                                                                                                                                                                                                                          Score 1144; DB 2; Length 770;
Pred. No. 2.2e-96;
1; Mismatches 4; Indels (
                        Indels
. 2.2e-96;
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                        Mismatches
           97.8%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                      Human STAT3 allelic variant
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Matches 224; Conservative
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                                                                            ACIGGPPNICLDRIENWITSLABSQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN
                     GNNQSVTRQXMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                   ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                  STAT; signal transducer and activator of transcription; crystal; drug design; murine.
                                                                                                           VELFRNIAKSAFVVEROPCMPMHPDRPLVIKTGVOFATAVALLVKFPEL 229
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/label= 3(10) helix of alpha helix
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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater than S.O Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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Copyright (c) 1993 - 2005 Compugen Ltd.
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IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
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US-08-276-099A-14
US-08-781-890-14
US-09-387-418A-15
US-09-387-418A-22
US-09-387-418A-22
US-09-387-418A-23
US-09-387-418A-10
US-09-387-418A-10
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US-09-430-86A-3
US-08-852-091-6
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APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzegzczynska, Melissa H
APPLICANT: Wrzegzczynska, Melissa H
APPLICANT: Horvath, Curr M
APPLICANT: Barnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
NUMBER OF SEQ ID NOS: 2.0
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US-09-387-418A-18
US-09-387-418A-18
Sequence 18, Application US/09387418A
Patent No. 6391572
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: WIZERZYJABKA, Melissa H
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Matches 229; Conservative
   ORGANISM: Mus musculus
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IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
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Pred. No. 8.6e-98;
0; Mismatches 3;
                                                                                                                         Sequence 9, Application US/09387418A;
Sequence 9, Application US/09387418A;
Patent No. 6391572;
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING;
CURRENT APPLICATION NUMBER: US/09/387,418A;
CURRENT FILING DATE: 1999-08-31
NUMBER: OF SEQ ID NOS: 43
SEQ ID NO 9
LENGTH: 271
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Best Local Similarity 98.7%;
Matches 226; Conservative
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GENERAL INFORMATION:

APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Horvath, Cutr M
APPLICANT: Horvath, Cutr M
APPLICANT: Horvath, Cutr M
APPLICANT: Horvath, Cutr M
APPLICANT: HORVATION: INTERACTIONS
FILE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
SUPPRESS OF FEQ ID NOS: 43
SUPPRESS OF FEG ID NOS: 43
SUPPRESS OF PATENTIN Ver. 2.0
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Pred. No. 7.6e-98;
0; Mismatches 3; Indels
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98.7%; Pred. No. 7.6e-98;
live 0; Mismatches 3;
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ilarity 98.7%;
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Best Local Similarity 98.7'
Matches 226; Conservative
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Best Local Similarity
Matches 226; Conserv
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US-09-387-418A-18
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GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zhong wen
APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPWLEERI 309
    190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
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                                             121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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                                                                                                                                                          310 VELFRNLMKSAFVVERQPCMPWHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                               181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 229
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Pred. No. 3.6e-97;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                  ; Sequence 12, Application US/08852091
; Patent No. 5883228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esg., David A. REGISTATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.7
Matches 226; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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US-08-852-091-12
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Patent No. 5716622

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Zilong Wen

APPLICANT: Zhong Zhong

TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL

TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
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                                                                                                                            61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                                             1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMODLN
                                                                    24 NHPTAAVVTEKQOMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMODLN
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  Gaps
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                                                                                                                                                                                                                                                                                                                                204 VELFRNIAKSAFVVERQPCMPWHPDRPLVIKTGVQFTTKVRLLVKFPEL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.8%; Score 1155; DB 1; Length 770; 98.7%; Pred. No. 3.6e-97;
  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 3.6e
0; Mismatches
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CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMUNICATION INPORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Klauber & Jackson STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Trans.
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TELEX: 133521
INFORMATION FOR SEQ 1D NO: 12: SEGUENCE CHARACTERISTICS: LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 770 amino acids amino acids
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Matches 226; Conservative
Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 07601
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Thu May 26 10:41:30 2005

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; MOLECULE TYPE: protein US-08-956-652-12
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                       310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
ITILE OF INVENTION: BECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY

ZIP: 07601

ZUP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 197/08/820,754
FILING DATE: 19-MAR-1997

***CATFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1155; DB 2;
Pred. No. 3.6e-97;
0; Mismatches 3;
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDRER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-MOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: WO MESSIVE APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-5EP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                               US-08-820-754-12
; Sequence 12, Application US/08820754
; Patent No. 5976835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.7%;
Matches 226; Conservative C
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121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                        250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                    VELFRNIMKSAFVVEROPCMPMHPDRPLVIKTGVOFATAVALLVKFPEL 229
                                                                                                                                                                                                                                                                     US-08-956-652-12
US-08-956-652-12
Sequence 12, Application US/08956652
Patent No. 6013475
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Ru, Xian-Yuan
APPLICANT: Wen, Zilong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
STRPPF
STRPPF
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FILING DATE: PRIGHT: US/08/956,652
FILING DATE: US/08/956,652
FILING DATE: US/08/956,652
FILING DATE: US/08/956,652
FILING DATE: US/08/9498
APPLICATION NUMBER: US 07/980,498
FILING DATE: 11-MAR-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/980,498
FILING DATE: US 07/854,296
FILING DATE: US 08/126,588
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gp. 600-1-073 CIP
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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TELEFAX: 201 487-5800
TELEFAX: 201343-1684
TELEX; 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
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Length 770;

DB 3;

98.8%; Score 1155;

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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFPNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                           190 GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
                                                                                                                                                                                                                                                                                                              61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                               250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                                                                                                                                                                                                                                                                                                                                                               121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                             1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                         Length 770;
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APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                             3; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
                                                                                                         Query Match 98.8%; Score 1155; DB 3; Best Local Similarity 98.7%; Pred. No. 3.6e-97; Matches 226; Conservative 0; Mismatches 3;
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: WO SPILORS
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NUMBER: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NUMBER: 24-SEP-1993
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6124118
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     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-869-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New Jersey
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US-08-948-547-12
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                                                                              1 NHPTAAVVTEKOOMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLLN
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                               Gaps
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APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong
APPLICANT: Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
Best Local Similarity 98.7%; Pred. No. 3.6e-97; Matches 226; Conservative 0; Mismatches 3; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,869
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APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION DATA: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson ESG., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 C.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/08956869
Patent No. 6030808
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APPLICATION NUMBER: 08/212,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
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INFORMATION FOR SEQ ID NO: 12:
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LENGTH: 770 amino acid
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
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US-08-956-869-12
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ZIP: 07601
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                                                                                                                                                                                                                                                                                                                                                                                      121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
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Sequence 3, Application US/09364970

Batent No. 6235873

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING FILE REFERENCE: 600-1-25

CURRENT APPLICATION NUMBER: US/09/364,970

CURRENT FILING DATE: 1999-07-31

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PATENTI VET: 2.0
                                                                                                                                                                                                                                                                                                                                         190 GNNQSVTRQKWQQLEQMLTALDQWRRSIVSELAGELLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                     1 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFDFNYKTLKSOGDMQDLN
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                                                                                                                                                                                     Score 1155; DB 3;
Pred. No. 3.6e-97;
0; Mismatches 3;
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Pred. No. 3.6e-97;
0; Mismatches 3;
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                                                                                                                                                                                       98.8%;
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acids
                                                                                                                                                                                                                      Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 226; Conservative
                                                                                                                 TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-948-547-12
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                                                                                                                                                                                                      Similarity
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Best Local Similarity
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Best Local
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250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                              GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
THILE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT APPLICATION NUMBER: 199-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
TITLE OF INVENTION: SECEPTOR RECGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SECRETOR BECCHINGS OF USE THEREOF
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,653A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1155; DB 3;
Pred. No. 3.6e-97;
0; Mismatches 3;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
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US-09-364-970-5; Sequence 5, Application US/09364970; Patent No. 6235873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.7
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-5
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STATE: New Jerse
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; Patent No. 6605442
; GENERAL INFORMATION:
   APPLICANT: Darnell Jr., James E.
   APPLICANT: Darnell Jr., James E.
   APPLICANT: Schindler, Christian W.
   APPLICANT: Wen, Zilong
   APPLICANT: Wen, Zilong
   APPLICANT: Wen, Zilong
   APPLICANT: Wen, Zilong
   APPLICANT: Poly Zhong
   APPLICANT: About RECEPTOR RECOGNITION FACTORS, PRU
   TITLE OF INVENTION: REQUENCES AND METHODS OF USE THEI
   TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEI
   ADDRESSEE: Klauber & Jackson
   STREET: 411 Hackensack Avenue
   CITY: Hackensack
   STATE: Mew Jersey
   COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                    PRIOR APPLICATION DAIRA
PRILICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: A-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 main o acid8
APPLICATION NUMBER: . US 07/980,498
FILING DATE: 23-NOV-1992
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Matches 226, Conservative
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MOLECULE TYPE: protein
                             FILING DATE: 23-NOV-1 PRIOR APPLICATION DATA:
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130 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 98.8%; Score 1155; DB 4; Length 770; Best Local Similarity 98.7%; Pred. No. 3.6e-97; Matches 226; Conservative 0; Mismatches 3; Indels
                              FILING DATE: 11-MAR-1994
CLASSIFICATION: 435
PROPERCATION NUMBER: 05 07/980,498
FILING DATE: 12-MOV-1992
PRICE APPLICATION DATA: 10-MAR-1994
FILING DATE: 19-MAR-1992
FILING DATE: 19-MAR-1992
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: 05 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESG., DAVIG A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
US/08/212,185
11-MAR-1994
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Job time : 28.6534 secs
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
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amino acid
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                                                             ; Search time 100.287 Seconds
  (without alignments)
763.830 Million cell updates/sec
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                                                                                                                              229
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Sequence 1
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Sequence 3
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1 NHPTAAVVTEKQQMLEQHLQ.....IKTGVQFATAVALLVKFPEL
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-090-185-18
US-10-090-185-14
US-10-090-185-14
US-10-090-185-14
US-10-090-185-9
US-10-090-185-31
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                                                                                                                                                                                    1434725 seqs, 334507595 residues
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Maximum Match 100%
Listing first 45 summaries
                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Sequence 149, App Sequence 12, Appl Sequence 12, Appl Sequence 23, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 2, Appl Sequence 1, Appl Sequence 1, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 15, Appl Sequence 15, Appl Sequence 14, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 16, Appl Sequence 16, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 780, App Sequence 780, App Sequence 329, App Sequence 550, App Sequence 24, Appl Sequence 6, Appli Sequence 8, Appli Sequence 4 US-09-925-302-780 US-09-925-302-780 US-10-116-275-329 US-10-106-185-19 US-10-090-185-15 US-10-090-185-15 US-10-090-185-15 US-10-090-185-22 US-10-090-185-23 US-10-090-185-16 US-10-090-185-17 US-09-876-773-4 US-10-245-120-1 US-10-308-579-44 US-10-755-889-352 US-10-455-889-823 US-10-492-043-19 US-110-639-617-4 US-10-090-185-24 US-09-876-773-8 US-09-833-205-6

ALIGNMENTS

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US-10-090-185-29

Sequence 29, Application US/10090185

Sequence 29, Application US/10090185

Sequence 29, Application US/10090185

Sequence 29, Application US/10090185

Shiblicant Information US/20020197647A1

SPECICANT: Zhang, Xiaokui

APPLICANT: Wrzeszczynska, Melissa H

APPLICANT: Wrzeszczynska, Melissa H

APPLICANT: Darnell Jr., James E

TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

TITLE OF INVENTION: METHODS FOR 10/10/090,185

TITLE OF INVENTION: UNBER: US/10/090,185

CURRENT APPLICATION NUMBER: US/10/090,185

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 29

LENGTH: 229
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Best Local Similarity 100.0%; Pred. No. 1.9e-94;
Matches 229; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                              CRGANISM: Mus musculus US-10-090-185-29
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ORGANISM:
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US-10-090-185-14

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sequence 14, Application US/10090185

sequence 14, Application US/20020197647A1

sequence 14, Application OS US20020197647A1

sequence 14, Application No. US20020197647A1

septicant: Areascaynska, Melissa H

APPLICANT: Paraell Jr., James E

septicant: Darnell Jr., James E

septicant Application NUMBER: US/10/090, 185

septicant Septicant NUMBER: US/387, 418

septicant NUMBER OF SEQ ID NOS: 43

septicant NUMBER Darnell Ver. 2.0

septicant No. 14

septicant N
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                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
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Pred. No. 3.2e-93;
0; Mismatches 3;
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Best Local Similarity 98.7%;
Matches 226; Conservative
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Matches 226; Conservative
                                ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-28
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LENGTH: 229
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; Sequence 28 Application US/10090185
; Publication No. US2002197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
FPLICANT: Darnell Jr., James B
TITLE OF INVENTION: MTHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR F
TITLE OF INVENTION: MTHODS FOR 1090,185
; CURRENT PERILON NUMBER: US/10/090,185
; CURRENT FILING DATE: 1999-08-31
; RIOR APPLICATION NUMBER: 09/387,418
; SOFTWARE: Patentin Ver: 2.0
; SEQ ID NO 28
                                                                                                                                                                                                                                                                                                      US-10-090-185-18

Sequence 18, Application US/10090185

Sequence 18, Application US/10090185

Publication No. US20020197647A1

GENERAL INFORMATION:
APPLICANT: Wizeczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: APPLICANT: WITHOUS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR F
TITLE OF INVENTION: INTERACTIONS
FILE REPERBNCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT APPLICATION NUMBER: 09/387,418
PRIOR PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43

SOFUMBER: PatentIn Ver. 2.0

SEQ ID NO 18

LENGTH: 229
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                                          ACIGGPPNICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
   ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
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Best Local Similarity 98.7%; Pred. No. 3.2e-93;
Matches 226; Conservative 0; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-18
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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.8%; Score 1155; DB 11; Length 770; 98.7%; Pred. No. 1.5e-92; ive 0; Mismatches 3; Indels 0
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Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON E8Q., David A.
REGISTRATION NUMBER: 26,742
TELECHONE: 201 487-5800
TELECHONE: 201 343-1684
                                            FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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Publication No. US20080079543A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 770 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Klauber
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STATE: New Jersey
COUNTRY: USA
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Matches 226; Conservative
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Sequence 9, Application US/10090185

Publication No. US20020197647A1

GENERAL INFORMATION:

APPLICANT: Zhang, Xiaokui

APPLICANT: Areascaynska, Melissa H

APPLICANT: Darnell Jr., James B

TITLE OF INVENTION: INTERACTIONS

FILE REPRENCE: 600-1-23

CURRENT APPLICATION NUMBER: US/10/090,185

CURRENT APPLICATION NUMBER: 09/387,418

PRIOR APPLICATOR NUMBER: 09/387,418

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOUTHWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: RECEPTOR RECCCNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 271;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1155; DB 13
Pred. No. 3.9e-93;
0; Mismatches 3
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ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/09876773
Publication No. US20040058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E. Schindler, Christian W. Fu, Xian-Yuan Wen, Zilong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 98.8%;
Best Local Similarity 98.7%;
Matches 226; Conservative (
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mus musculus US-10-090-185-9
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US-09-876-773-12
                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 9
LENGTH: 271
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IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
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                                                                                                     Length 229;
                                                                                                                                                     Indels
                                                                                                  Score 1151; DB 13;
Pred. No. 7.1e-93;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Mrzeszczynska, Melissa H
APPLICANT: Mrzeszczynska, Melissa H
APPLICANT: Darnell Jr., James
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
FILE REFERENCE: 600-1-253
FILE REFERENCE: 600-1-253
FILE REFERENCE: 000-1-253
FILE REFERENCE: 000-1-253
FILE REFERENCE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-090-185-30
; Sequence 30, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
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US-10-380-020-4
; Sequence 4, Application US/10380020
                                                                                                  Query Match
Best Local Similarity 98.3%;
Matches 225; Conservative
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Matches 225; Conservative
                              ; ORGANISM: Mus musculus
US-10-090-185-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
                                                                                                Query Match
Best Local Similarity
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     TYPE: PRT
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Publication No. US20020197647A1

GENERAL INFORMATION:

APPLICANT: Zhang, Xiaokui

APPLICANT: Arzeszczynska, Melissa H

APPLICANT: Horvarh, Outr M

APPLICANT: HORVARION:

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

CURRENT APPLICATION NUMBER: US/10/090,185

CURRENT APPLICATION NUMBER: 09/387,418

PRIOR PLILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFUTARE: Patentin Ver: 2.0

SEQ ID NO 31

LENGTH: 229
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 98.8%; Score 1155; DB 17 Best Local Similarity 98.7%; Pred. No. 1.5e-92; Matches 226; Conservative 0; Mismatches 3
                                                                                                             APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-MOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY AGENT INFORMATION:
                         APPLICATION NUMBER: US/10/639,617
FILING DATE: 12-Aug-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-10-639-617-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 770 amino acids
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Pardoll, Drew
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stat 3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-9990
CURRENT APPLICATION NUMBER: US/10/380,020
CURRENT APPLICATION NUMBER: 60/231,212
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 769
    250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPWLEERI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                                            ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 5, Application US/10380020; Publication No. US20040052762A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/10045792
Publication No. US20030003563A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo Sapiens
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                                                                        APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Dardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Star3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REPERBNCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
PURRENT FLING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR FILING DATE: 2000-09-08
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APPLICANT: PardOll, Drew
APPLICANT: Dave All the APPLICANT: Jove, Richard
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
PRIOR APPLICATION NUMBER: G0/231,212
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.9%; Score 1144; DB 15; Length 720; 97.8%; Pred. No. 1.3e-91; ive 1; Mismatches 4; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
SEQ ID NO LENGTH: 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 15
SOFWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 769
Publication No. US20040052762A1 GENERAL INFORMATION:
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Best Local Similarity 97.8°
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo Sapiens
US-10-380-020-4
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US-10-380-020-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMBYVQKTLTDEELADWKRRPEI
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Publication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFRENCE: B4767A
CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT FILING DATE: 2002-07-23
PRIOR PILING DATE: 2001-01-02
NUMBER OF SEQ 1D NOS: 67
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                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-0ct-2001
CLASSIFICATION = Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
FILING DATE: cUnknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEFAX: 201-343-1684
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-045-792-8
                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SECTIONO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acids
STRANDEDNESS: single
ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
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ORGANISM: Homo sapiens
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LENGTH: 770
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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                                                                                                             Length 770;
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                                                                                                                                                                                                                                                        4; Indels
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; Sequence 2, Application US/10117087
; Publication No. US20030166854A1
; GENERAL INFORMATION:
; APPLICANT: SERLUPI-CRESCENZI, Ottaviano
; APPLICANT: DELLA PIETRA, Linda
; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
; FILE REPERENCE: SERLUPI=2
; CURRENT APPLICATION NUMBER: US/10/117,087
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US/09/526,542
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 770
                                                                                                                                                                                          Score 1144; DB 14;
Pred. No. 1.4e-91;
1; Mismatches 4;
; FEATURE:
; NAMEKEY: STAT3 : Transcription factor
; LOCATION: (1)..(770)
; OTHER INFORMATION:
US-10-038-010-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: May 25, 2005, 18:21:53
Job time : 101.62 secs
                                                                                                                                                                                       Query Match 97.9%;
Best Local Similarity 97.8%;
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 25, 2005, 17:24:07 ; Search time 21.6038 Seconds (without alignments) 1019.898 Million cell updates/sec Run on:

Title: Perfect score:

US-10-090-185-29 1169 1 NHFTAAVVTEKQQMLEQHLQ.....IKTGVQFATAVALLVKFPEL 229 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	-
Result No.	Score	Query Match	Length	DB	ID	Description
٦	1144	97.9	770		I49508	ISGF3 p91-related
73	1139	97.4	770	~	A54444	DNA-binding protei
3	510.5	43.7	739	~	A46159	interferon-depende
4	495	42.3	748	7	A56047	gamma-interferon a
S	310	26.5	851	~	A46160	interferon alpha-i
9	269.5	23.1	786	7	149274	mammary gland fact
7	269.5	23.1	793	~	S54772	
80	263.5	22.5	794	7	G02317	transcription acti
6	238	20.4	794	~	S55527	
10	126	10.8	978	~	A70387	conserved hypothet
11	124	10.6	533	7	G72593	hypothetical prote
12	122	10.4	848	~	A54740	interleukin-4-indu
13	120.5	10.3	837	7	157557	DNA-Binding Protei
14	119.5	10.2	1166	~	T27075	hypothetical prote
15	118.5	10.1	1208	N	AE1947	chromosome segrega
16	118.5	10.1	2094	N	833124	tpr protein - huma
17	115.5	9.9	924	~	806117	myosin heavy chain
18	115	9.8	1164	~	T24806	hypothetical prote
19	114.5	9.8	2007	~	B43402	myosin heavy chain
20	114	9.8	1976	~	A59252	myosin heavy chain
21	113.5	6.7	727	~	AC1814	hypothetical prote
22	113.5	9.7	857	~	S33821	median body protei
23	112.5	9.6	946	N	S28061	SCP1 protein - rat
24	112.5	9.6	1690	~	T13030	microtubule bindin
25	112.5	9.6	1957	7	T38077	hypothetical coile
26	112.5	9.6	2253	~	T30336	nuclear/mitotic ap
27	112	9.6	289	~	S51193	epimorphin - mouse
28	112	9.6	1509	H	A27224	heavy
29	112	9.6	1999	H	S21801	myosin heavy chain

M protein - Helico	exonuclease (EC 3.	myosin heavy chain	kinesin-related pr	myosin heavy chain	myosin heavy chain	chromosome segrega	hypothetical prote	hypothetical prote	myosin heavy chain	hypothetical prote	epidermal growth f	ATP-dependent dsDN	ATP-dependent dsDN	interaptin - slime	dystrophin, muscle
C64527	BVECSC	A33977	A57107	A59287	A47297	G83960	T21174	T43448	833068	T27055	S43074	C85535	G90684	T14867	A27605
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284	1048	1959	747	1940	1992	1188	2020	434	527	734	968	1047	1047	1738	3685
9.5	9.5	9.5	9.5	9.5	9.5	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4
111.5	111.5	111	110.5	110.5	110.5	110	110	109.5	109.5	109.5	109.5	109.5	109.5	109.5	109.5
30	31	32	33	, 7,	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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97.9%; Score 1144; DB 2; Length 770;
Best Local Similarity 97.8%; Pred. No. 1e-68;
Matches 224; Conservative 1; Mismatches 4; Indels
149508
ISGF3 p91-related transcription factor - mouse
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RESULT 2 A54444 DNA-binding protein APRF - human

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A;Cross-references: EMBL:U18671; NID:g1293919; PIDN:AAA98760.1; PID:g1293920
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
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Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
Affitle: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa ISG
A;Reference number: A46159; MUID:92366557; PMID:1502203
A;Accession: A46159
C;Species: Homo sapiens (man)
C;Date: 2.1-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: A54444
R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sud
Call 77, A3-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tra
A;Reference number: A54444; MUID:94208062; PMID:7512451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPPNICLORLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELF 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Homo sapiens (man)
Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004; Accession: A46159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 ACIGGPPNICLDRLENWITSLAESQLOTRQOIKKLEELHQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLNGNNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNNOSVTROKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                       A,Accession: A54444
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Rosiduss: 1-770 <RES>
A;Cross-references: UNIPROT:P40763; GB:L29277; NID:G475788; PID:G475789
GGenetics:
A;Gene: GDB:STAT3; APRF
A;Cross-references: GDB:358950
A;Amap postition: 17421-17421
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Experimental source: HeLa cells Note: sequence extracted from NCBI backbone (NCBIP:110818) Superfamily: human signal transducer and transcription activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 739;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid; protein A;Residues: 1-739 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.7%; Score 510.5; DB 2; Length 44.9%; Pred. No. 1.4e-26; Live 49; Mismatches 62; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1139; DB 2;
Pred. No. 2.3e-68;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPROT: P42224
                                                                                                                                                                                                                                                                                                                                                                                                                                            97.4%;
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Best Local Similarity
Matches 101; Conserva
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Best Local Similarity
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C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56047
R;Accession: A56047
R;Yamamoto, K; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, Mol. Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in e. A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Accession: A56047
A;Reinland: A;Molleule type: mRNA
A;Residues: 1-748 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P42228; GB:U09351; NID:9509502; PIDN:AAA19692.1; PID:950950
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferon alpha-induced transcription activator ISGF-3, 113K chain - human NyAlternate names: stat2 protein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 2.1-Sep-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46160; S71908; S53873
B;Fu, X.Y.; Schindler, C.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator A;Reference number: A46160; MUID:92366558; PMID:1502204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPNICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 PLHNGLDQLQNCFTLLABSLFQLRQQLBKLQBQSTKWTYBGDPIPAQRAHLLBRATFLIX 309
-QVRQQLKKLEELEQKYTYEHDPITKNKQVLWDRTFSLF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 VTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKS--QGDMQDLNGNNQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 748;
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                                                                                                                                                                                                                                                                                                                 gamma-interferon activation site-binding protein Stat4 - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68; Indels
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                                                                                                               185 RNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.3%; Score 495; DB 2;
44.2%; Pred. No. 1.6e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 44.29
   250 GPPNACLDQLQ---
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A; Residues: 1-851 < YAN>
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63

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mammary gland factor - mouse

NyAlternate names: stat5 protein
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S54772; 149273
R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
BMBO J. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin A;Reference number: S54772; MUID:95237198; PMID:7720707
A;Accession: S54772
A;Status: preliminary, nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-793 <MUI>
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A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved A;Reference number: 149273; MUID:96004632; PMID:7568026
                                                                                     13.7 MSQKHLQINQRPBELRLITQDTENELKKLQQTQEYFIIQYQESLRIQAQPAQLGGLNPQE 196
                                                                                                                                                                                                                                                                                     194 PQERMSRETALQQKQVSLETWLQREAQTLQQYRVELAEKHQKTLQLLRKQQTIILDDELI 253
                                                                                                                                                                                                                                                                                                                                                                      113 DWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQH 172
                                                                                                                                                                                                                                                                                                                                                                                                                     254 QWKRRQQLAGNGGPPEGSLDVLQSWCEKLAEIIWQNRQQIRRAEHLCQQLPIPG-PVEEM 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 RMSRETALOOKOVSLETWLOREAQTLOOYRVELAEKHOKTLOLLRKOOTIILDDELIOWK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 RRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPM 175
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C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
                                                   AAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNY-KTLKSQGDMQDLNGNN
                                                                                                                                                                                                        -----QSVTRQKMQQLEQML----TALDQMRRSIVSELAGLLSAMEYVQKTLTDEELA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 LAEVNATITDIISALVTSTFIIEKQP------PQVLKTQTKPAATVRLLV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 RPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 LEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLV 224
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A; Regidues: 1-793 <RES>
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                                                                A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Cross-references: EMBL:U18671
C;Genetics:
A;Gene: stat2
A;Introns: 44/2; 95/3; 127/3; 183/1; 211/3; 261/2; 314/2; 345/2; 365/2; 372/2; 46
C;Superfamily: human signal transducer and transcription activator STATSA
C;Keywords: signal transduction; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-786 <RES>
A; Residues: 1-786 <RES>
A; Cross-references: UNIPROT: P42232; UNIPROT: 09JKM1; EMBL: U21110; NID: 9747973; PiDN: AAG52
R; Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
A; Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
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Afacession: S54773
Afacession: S64773
Afaceule type: mRNA
Afaceule type: mVI
Afaceule type: mV
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A,Reference number: S54772; MUID:95237198; PMID:7720707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NiAlternate names: STATS protein homolog p80
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: O2-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149274; S54773; S54727
R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved A;Reference number: 149273; WUID:96004632; PMID:7568026
A;Accession: 149274
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROKMOOLEQMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEIACIGGPP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 NICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNL 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Match 26.5%; Score 310; DB 2; Length 851; Local Similarity 32.6%; Pred. No. 3.7e-13; les 72; Conservative 51; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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A; Reference number: S53873; MUID:95192056; PMID:7885841
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                                      A; Accession: S53873
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5,

Gaps

21;

Length 793;

us-10-090-185-29.rpr

C;Accession: G02317 R;Lin, J. submitted to the EMBL Data Library, December 1995 A;Reference number: H01043	Qy 176 LEERIVELFRNLMKSAFVVBRQPCMPMHPDRPLVIKTGVQFATAVALLV 224
A;Accession: G02317 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-794 <lin> A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:g1151169; PIDN:AAB06589.1; PID:g115 C;Superfamily: human signal transducer and transcription activator STATSA</lin>	RESULT 10 A70387 conserved hypothetical protein aq 1006 - Aquifex aeolicus C;Species: Aquifex aeolicus
Query Match 22.5%; Score 263.5; DB 2; Length 794; Best Local Similarity 30.1%; Pred. No. 4.3e-10; Matches 69; Conservative 43; Mismatches 96; Indels 21; Gaps 5;	<pre>C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004 C;Accession: A70387 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Or V.</pre>
8 VTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNY-KTLKSQCDMQDL 59 :::	Nature 392, 353-358, 1998 A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Reference number: A70300; MUID:99196666; PMID:9537320 A,Accession: A70387
OY 60 NGNNOSYTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMBYVQKTLTDEELADWK 115	A;Status: preliminary; nucleic acid sequence not snown; translation not snown A;Molecus type: DNA A;Molecus: 1-978 <aqf> A;Residues: 1-978 <aqf> A;Cross-references: UNIPROT:067124; GB:AE000718; NID:g2983504; PIDN:AAC07092.1; PID:g29:</aqf></aqf>
QY 116 RRPEIACIGGPRNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDFIVQHRPM 175	A.Experimental Bource: Strain vro C.Genetics: A,Gene: aq_1006 C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032
Qy 176 LEERIVELFRNIMKSAFVVERQECMPMHPDRPLVIKTGVQFATAVALLV 224 : : : : :	Query Match Best Local Similarity 23.8%; Pred. No. 0.77; Matches 50; Conservative 38; Mismatches 80; Indels 42; Gaps 6;
RESULT 9 SS5527 SS5527 Annual factor choose	OY 10 EKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDBPDFNYKTLKSQGDMQDLNGNNQSVTRQ 69 :: : : :
mammary land land land land land (Species: Ovis or land) (Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep) (Species: Ovis orientalis aries, Ovis ammon 03-Nov-1995 #text_change 09-Jul-2004 (Species: Species) (Species: Species) (Species: Ovis orientalisms) (Spec	Oy 70 KWOQLEQMITALDQMRRSIVSELAGLLSAMEYVQKTLTDEELAD- 113 :::::::
Aymondo, 14, 854-855, 1995 A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regula A;Reference numbers. S55527; MUID:95188889; PMID:7882987	OY 114 WKRRPEIACIGGPPNICLDRLENWITSLAESOLGTRQQIKKLEELQQKVSYKGDPIVQHR 173
A.Molecule type: mRNA A.Molecule type: mRNA A.Cross-references: UNIPROT: P42231; EMBL:X78428; NID:g602354; PIDN:CAA55191.1; PID:g6023 A.Note: this is a revision to the sequence from reference 844353	Oy 174 PMLEERIVELFRNLMKSAFVVERQ 197 Db 394 EEKLEKIKELFSEBEYTSLKMKERLLVELQ 423
R,Wakao, H.; Gouilleux, F.; Groner, B. EMBO J. 13, 2182-2191, 1994 A;Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcri A;Reference number: S44353; MUID:94244619; PMID:7514531	ESULT 172593 Ypothet
A;Accession: S44353 A;Molecule type: mRNA A;Residues: 1-716,'RHLHGPGSLPSR',729,'P',731,'ASL' <waw> A;Crose-references: ENBL:X78428</waw>	C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004 C;Accession: G72593 R;Kawarabayasi, Y.; Hino, Y.; Horikawa. H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka
reference S55527 d transcription act	awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
Query Match 20.4%; Score 23%; DB 2; Length 794; Best Local Similarity 29.3%; Pred. No. 2.1e-08; Matches 67; Conservative 42; Mismatches 98; Indels 22; Gaps 6;	A; Reference number: A72450; MUID: 99310339; PMID: 10382966 A; Accession: G72593 A; Struus: preliminary A; And coning troop on the contract of
QY 8 VTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNY-KTLKSQGDMQDLNGNN 63 :::	A, Residues: 1-533 <kgw> A, Residues: 1-533 <kgw> A, Cross-references: UNIPROT:Q9YCP2; DDBJ:AP000061; NID:g5104821; PIDN:BAA80205.1; PID:d A, Experimental source: strain Kl</kgw></kgw>
QY 64QSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWK 115 DD 198 RLSRETALQQKQVSLEAWLQREAQTLQQYRVSLAEKHQKTLQLLRKQQTIILDDELIQWK 257	A; Gene: APE1216 Query Match 10.6%; Score 124; DB 2; Length 533;
RRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPM 17	Best Local Similarity 21.2%; Pred. No. 0.52; Matches 42; Conservative 49; Mismatches 65; Indels 42; Gaps
DD Z38 KKHUWKGWEAFFK-SLDVLLQSWCENLABIIWQNKQQIKKAEHLCQQLFIFG-FVEEMLAB 315	QY 8 VIEKQQMLEQHLQDVKKKVQDLEQKMKVVENLQDDF-;DFNIK 48

); S.M.; Cleve	Query Match 10.18; Score 120.5; DB 2; Length 837; Match Match
A;Accession: 15/55/ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-837 <res> A;Crost-references: UNIPROT:P52633; GB:L47650; NID:g1008876; PIDN:AAA79006.1; PID:g10088 C;Genetics: A;Gene: STAT6 C;Superfamily: human signal transducer and transcription activator STAT5A</res>	RESULT 15 AE1947 Chromosome segregation protein [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
A)NA Res. 8, 205-213, 2001
A)Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                       A;Residues: 1-1208 «KUR»
A;Cross-references: UNIPROT:Q8YXT3; GB:BA000019; PIDN:BAB73085.1; PID:g17130474; GSPDB:G
A;Experimental source: strain PCC 7120
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1014 ALEEYERTQKRLBELSQKLQTLGGE----RTELLLRI-ENFTTLRQIAF 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 -----KKLEELQQKV-SYKGDPIVQHRPMLEERIVELFRNLMKSAF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 23.9%; Pred. No. 3.1;
Matches 55; Conservative 44; Mismatches 82; Indels 49;
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A,Gene: alr1128
C,Superfamily: chromosome segregation protein SMC1
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C; Accession: AE1947
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TISSUE=Placenta; Machael Tissue Trissue Trissue Trissue Trissue Machael Trissue Trissu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.
Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
Rajkumar N., Yi Q., Nickerson D.A.;
"SeattleSNPs. NHLBI Hi6682 program for genomic applications, UW-
FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;
"Highly conserved amino-acid sequence between murine STAT3 and a
revised human STAT3 sequence.";
Gene 213:119-124(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                      STA3_HUMAN STANDARD; PRT; 770 AA.
P40763; 014916; Q9BW34;
01-FEB-1995 (Rel. 31, Created)
05-UTL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase
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08JFU8
0801X2
STA4 HUWAN
090VI
013132
013132
073253
072253
072257
08AW20
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08JFU7
08JFES5
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Homo sapiens (Human).
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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STA3_MOUSE
STA3_RAT
STA3_BOVIN
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Maximum Match 100%
Listing first 45 summaries
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GO:0005634; C:nucleus; TAS.
GO:0005062; F:hematopoietin/interferon-class (D200-domain. . .; TAS.
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=11773079; DOI=10.1074/jbc.M111486200; PubMed=11773079; DOI=10.1074/jbc.M111486200; Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.; Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.; Trunctional interaction of STAT3 transcription factor with the coactivator NcoA/SRC1a."; J. Biol. Chem. 277:8004-8011(2002).

-I. FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6) responsive elements identified in the promoters of various acute-phase protein genes.
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-1-TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas.
-1- FTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity.
-1- SIMILARITY: Belongs to the transcription factor STAT family.
-1- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95215843; PubMed-7701321; Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.; Requirement of serine phosphorylation for formation of STAT-promoter complexes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: Involved in the gpl30-mediated signaling pathway.
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOAI.
-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                      Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O., Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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EMBL, AY572796, AAS66986.1,
EMBL, BC000627, AAH00627.1,
EMBL, BC014482, AAH14482.1,
EMBL, AF029311; AAB84254.1;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 564-704 FROM N.A.
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Genew; HGNC:11364; STAT3.
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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPWLEERI 309
R GO; GO:0003700; F:transcription factor activity; TAS.
R GO; GO:0007259; P:cell motility; TAS.
GO; GO:0007259; P:JAK-STAT cascade; TAS.
GO; GO:0000122; P:DAFE STAT cascade; TAS.
GO; GO:0007185; P:Bagnal transduction; TAS.
GO; GO:0007165; P:signal transduction; TAS.
R GO; GO:0007165; P:signal transduction; TAS.
R InterPro; IPR000980; SH2.
R InterPro; IPR001217; STAT.
R Pfam; PF00107; STAT alpha; 1.
R Pfam; PF02864; STAT lint; 1.
R Pfam; PF02865; STAT lint; 1.
R Pfam; PF02865; STAT lint; 1.
R PROSTE; PS50001; STAT lint; 1.
R PKGSTTE; PS50001; STAT lint; 1.
W Activator; Alternative splicing; DNA-binding; Nuclear protein;
M PROSPORTITE; PS50001; STAT lint; 1.
W PROSTITE; PS50001; STAT lint; 1.
W PROSTITE; PS50001; STAT lint; 1.
W PROSTITE; PS50001; STAT lint; 1.
                                                                     . .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNNQSVTROKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
                                                                                                                                                                                                                                                                                                                                                                                        Phosphotyrosine (by JAK) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND 632-640.
STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-21004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 97.9%; Score 1144; DB 1; Length 770; Local Similarity 97.8%; Pred. No. 4.3e-62; les 224; Conservative 1; Mismatches 4; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                Phosphoserine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                Missing (in isoform Del-701)
/FTId=VSP 010474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F -> Y (in Ref. 1).
V -> L (in Ref. 1).
T -> A (in Ref. 1).
; 6C00632211C8012D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O -> K (in dbSNP:1803125)
/FIId=VAR_018683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q -> H (in Ref. 1)
P -> S (in Ref. 1)
K -> N (in Ref. 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M -> I.
/FTId=VAR
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Name=Stat3; Synonyms=Aprf;
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667
730
770 AA;
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727
701
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P42227;
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MOD_RES
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STRAIN-EVBN/N; TISSUE-Mammary gland;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Astaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A.M., Rouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rotiguez A.C., Gimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Bronnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                      MEDLINE=95014185; PubMed=7523373;
Raz R., Durbin J.E., Levy D.E.;
"Acute phase response factor and additional members of the interferon-stimulated gene factor 3 family integrate diverse signals from cytokines, interferons, and growth factors.";
J. Biol. Chem. 269:24391-24395(1994).
Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T., Yoshida K., Sudo T., Naruto M., Kishimoto T.; "Molecular cloning of ARRF, a novel IRW-stimulated gene factor 3 p91-related transcription factor involved in the gp130-mediated signaling
                                                                                                                                               Zhong Z., Wen Z., Darnell J.E. Jr., "Stat3: a STAT family member activated by tyrosine phosphorylation in response to epidermal growth factor and interleukin-6."; Science 264:95-98(1994).
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM STAT3B).
STRAIN=BALB/c, and CS7BL/6; TISSUB=Liver;
MEDLINE=96016116; PubMed=7568080;
Schaefer T.S., Sanders L.X., Nathans D.;
"Cooperative transcriptional activity of Jun and Stat3 beta, a short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J, and NOD/LtJ;
Davoodi-Semiromi A., She J.-X.;
A mutant Stat5b with weaker DNA binding defines a key defective pathway in non-obese diabetic (NOD) mice.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11161808; DOI=10.1006/geno.2000.6433;
Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T.,
Dewar K., Hennighausen L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.
                                                                                                       SEQUENCE FROM N.A. (ISOFORM STAT3A).
                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM STAT3A).
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                                                                                                                                    MEDLINE=94188718; PubMed=8140422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 71:150-155(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zebrafish to mouse.";
                                                                         Cell 77:63-71(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/SvJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                            form of Stat3.
                                                                                                                                                                                                                                             TISSUE=Brain;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IL-6)-responsive elements identified in the promoters of various acute-phase protein genes. STAT3B interacts with the N-terminal part of JUN to activate such promoters in a cooperative way.

-!- PATHWAY: Involved in the gpl30-mediated signaling pathway.
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).
-!- SUBCELLUAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.
-!- ALTERNATIVE PRODUCTS:
-!- ALTERNATIVE PRODUCTS:
-!- ALTERNATIVE PRODUCTS:
MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9; Wen Z., Zhong Z., Darnell J.E. Jr.; Wen Z., Zhong Z., Darnell J.E. Jr.; Waximal activation of transcription by Statl and Stat3 requires both tyrosine and serine phosphorylation."; Cell 82:241-250(1995).
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The structure of struct
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                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
MEDLINE-89334373; PubMed=9671298; DOI=10.1038/28101;
Becker S., Groner B., Medller C.W.;
"Three-dimensional structure of the Stat3beta homodimer bound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pro.
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R. EMBL; U08378; AAA56688.1; -..

R. EMBL; U33709, AAC52612.1; -..

R. EMBL; A7299489; AAC52612.1; -..

R. EMBL; A7299489; AAC52612.1; -..

R. EMBL; A7299489; AAC75418.1; -..

R. EMBL; A7299489; AAQ75418.1; -..

R. EMBL; A7299489; AAQ75418.1; -..

R. EMBL; BC039400; AAQ75418.1; -..

R. EMBL; BC039400; AAQ75418.1; -..

R. EMBL; BC039400; AAQ75418.1; -..

R. EMBL; BC03940; AAQ75418.1; -..

R. EMBL; BC03940; AAQ75418.1; -..

R. EMBL; BC0340006; AAH03806.1; -..

R. GO; GO:0005737; C:Cytoplasm; IDA.

R. GO; GO:0005737; C:Cytoplasm; IDA.

R. GO; GO:0005886; C:plasma membrane; IDA.

R. GO; GO:0005886; C:plasma membrane; IDA.

R. GO; GO:0005886; C:plasma membrane; IDA.

R. GO; GO:0005588; C:plasma membrane; IDA.

R. GO; GO:0005589; P:DAX-STAT cascade; IDA.

R. GO; GO:0007259; P:JAX-STAT cascade; IDA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 394:145-151(1998).
-!- FUNCTION: Transcription factor that binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Stat3B;
IsoId=P42227-2; Sequence=VSP_006287;
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InterPro; IPR001980; SH2.
InterPro; IPR001217; STAT.
PFam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF01064; STAT_bhind; 1.
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MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                               61 GNNOSVTROKMOQLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPBI 120
                                                                                                                                                                                                                                                                                                                                                                        121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                      Phosphotyrosine (by JAK) (By similarity).
                                                            Phosphoserine.
TTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
                                                                                                                                                                                                                                                                                                                                 1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                            FDMDLTSECATSPM -> FIDAVWK (in isoform
                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                          181 VELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFATAVALLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (In isoform Del-701).
/FyrdavSp 010475.
S-A: Decreased transcriptional activation:
                                                                                                                                                                                                                                                                                                    97.9%; Score 1144; DB 1; Length 770; 97.8%; Pred. No. 4.3e-62; ive 1; Mismatches 4; Indels (
Pfam, PF02865; STAT int; 1.
PROSITE; PS50001; SH2; 1.
3D-structure; Activator; Acute phase; Alternative splicing; Direct protein sequencing; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain; Transcription regulation.

Frosphorylation; SH2 domain; Transcription (by JAK) (By s
                                                                                                                               -> K (in Ref. 2).
-> T (in Ref. 2 and 4).
-> I (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
02-0CT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
Name=Stat3;
                                                                                          FTId=VSP 006287
                                                                                     Stat3B)
                                                                                                                                                                                                                                                                                                           Best Local Similarity 97.8
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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P52631;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                     "Transcription factors Stat3 and Stat5b are present in rat liver nuclei late in an acute phase response and bind interleukin-6 response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACIDETA PARTIES TO CONTROLL OF THE PRODUCTS OF WALTON CALLY TO THE PRODUCTS OF WALTON CALLY TO THE ACID OF WALTON CALLY TO THE ACT OF THE ACID OF WALTON CALLY OF THE ACID OF 
                                                                                                                                                                                                                                                                                                                       elements.";
J. Biol. Chem. 270:29998-30006(1995).
J. Biol. Chem. 270:29998-30006(1995).
-!- FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
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Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
SWART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
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MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998;
Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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InterPro; IRR008967; P53 like_DNA_bnd.
InterPro; IRR0008960; SH2...
InterPro; IPR001217; STAT.
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DOMAIN 580 670
MOD RES 705 705
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Name=stat 3;
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphotyrosine (by JAK) (By similarity)
Phosphoserine (By similarity).
9CEB147C73E83274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.3%; Score 1137; DB 1; Length 770; 97.4%; Pred. No. 1.1e-61; ive 1; Mismatches 5; Indels
                            05-UUL-2004 (Rel. 44, Created)
05-UUL-2004 (Rel. 44, Last sequence update)
05-UUL-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Name=STAT3;
                                                                                                                                                                    TISSUE-Nammary gland;
Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
         770 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ620655; CAF06182.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87974 MW;
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Transcription regulation.
DOMAIN 580 670
MOD_RES 705 705
MOD_RES 727 727
CEVITENCE 770 AA; 87974 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 97.4 Matches 223; Conservative
         STANDARD;
                                                                                       Bos taurus (Bovine).
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                        Bovinae, Bos.
NCBI_TaxID=9913;
         BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310
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Ā 771

PRT;

PRELIMINARY;

Q6DV79; Q6DV79

RESULT 5 06DV79 ID 06 AC 06

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131 HPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQCDMQDLNG 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 CIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIV
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                                                                                           vallus galius (Ultoren).
Eukaryota; Metazoa; Choridata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gabe
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MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
Asashina M., Yokota T.;
"Activation of Stat3 by cytokine receptor gpl30 ventralizes Xenopus
embryos independent of BMP-4.";
Dev. Biol. 216:481-490(1999).
EMBL; AB017701; BAA86061.1; -.
                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 771;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88174 MW; 71AC855C5DEC03E2 CRC64;
                     Last sequence update)
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Last annotation update)
                                                             Signal transducer and activator of transcription 3. Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1119; DB 2;
Pred. No. 1.5e-60;
1; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 694
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR008967; P53_like_DNA_bnd
InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.7%;
25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 96.1
es 219; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS50001; SHZ;
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NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            771 AA;
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Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                         Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 208; Conservative
                             cDNA sequences
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                                                                                               SEQUENCE FROM N.A.
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                             mouse
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shaneme C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Stapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheefz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Robards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Willalon D.K., Muxry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Kraywinski M.I., Salaleka U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 SHPNAAVVTEKQQMLEQHLQDVRKKVQDLEQKWKVVENLQDDFDFNYKTLKSQSDLSELN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 GNNQSVTRQXMQQLEQMLTALDQLRRTIISDLASLLSAMEYVQXTLTDEELADWKRRQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 ACIGGPPNICLDRLENWITSLAESQLQIRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                   GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; F93_like_DNA_bnd.
InterPro; IPR001217; STAT.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.9%; Score 1086; DB 2; Length 769; 91.7%; Pred. No. 1.5e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Indels
                                                                                                                                                                                                                                                                                                                                                           0905C03263303069 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                               Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
PROSTTE; PS50001; SH2; 1.
PROSTTE; PS50001; SH2; 1.
SEQUENCE 769 AA; 87974 MW; 09
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072XX3;
01-UNN-2003 (TrEMBLrel. 24, Lc)
01-UNN-2003 (TrEMBLrel. 24, Lc)
01-MAR-2004 (TrEMBLrel. 26, Lc)
Stat3-A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 91.7
Matches 210; Conservative
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NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Q7ZXK3
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121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
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                                                                                                                                                                                                                                                                                                                                                                                             SHPNAAVITEKQQMLEQHLQDVRKKVQDLEQKMKVVENLQDPDFNYKTLKSQSDLSELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Daniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
ACBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                         TISSUE=Embryo;

BEDLINE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

Richardson P.;
                                                                                                                                                                    Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.6%; Score 1083; DB 2; Length 766; 90.8%; Pred. No. 2.3e-58; ive 11; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Embryo;
TISSUE=Embryo;
Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC044717; AAH44717.1;
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     766 AA; 87599 MW; 31018A3321CCEB9C CRC64;
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Last annotation update)
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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189

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R., Hong
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               Straubberg R.L., Feingold E.A., Grouse L.H., Derge JG.,

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge JG.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A ltschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Heieh F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Mitting M. M. Gobergren E.J., Lockson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IACIGGPPNICLDRLENWITSLAESQLQTRQQIKXLEELQQKVSYKGDPIVQHRPMLEER 179
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                                                                                                                                                                                                                                                                                                                                                                                                                           Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 HPTAAVVTEKQOMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
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GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:00006355; P:signal transduction; IEA.
InterPro; IPR008967; P53 like DNA bnd.
InterPro; IPR008967; P53 like DNA bnd.
Ffam; PF01017; STAT alpha; 1.
Ffam; PF02864; STAT lint; 1.
Ffam; PF02865; STAT Lint; 1.
SEQUENCE 414 AA; 48253 WW; OFFD1BS09B7526BD CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Signal transducer and activation of transcription factor 3.
Oryzias latipes (Medàka fish) (Japanese ricefish).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ruteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 IVDLFRNIAKSAFVVERQPCMPWHPDRPLVIKTGVQFTTKVRLLVKFEL 359
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO45277; AAH45276.1; -.
HSSP; P42227; 1BG1.
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83.5%; Pred. No. 1.9e-53;
ive 21; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse cDNA sequences."
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Matches 192; Conservative
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RAYARA RA
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250 IACIGGPPNICLDRLETWITSLAESQLQIRQQIKKLEELQQKVSYKGDPIIQHRPALEEK 309
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Liu R., Hong Y.;
Liu Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AV641434; AAT46164.1;
EMBL, AV641434; AAT46164.1;
R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0007242; C:nucleus; IEA.

R GO; GO:0007242; P:intracellular signaling cascade; IEA.

R GO; GO:0007242; P:intracellular signaling cascade; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR0019967; PF3_like_DNA_bnd.

R InterPro; IPR00117; STAT.

R Pfam; PF001017; STAT.
                                                                                                                                                                                                                                                                                                                                                                            L; AY639947; AAT64912.1; -.. GO:0005634; C:nucleus; IEA. GO:0005634; C:nucleus; IEA. GO:0004871; F:signal transducer activity; IEA. GO:0003700; F:transcription factor activity; IEA. GO:0007242; P:intracellular signaling cascade; IEA. GO:000555; P:regulation of transcription, DNA-dependent; IEA.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation 3 isoform 1.
07-Zias latipes (Medaka fish) (Japanese ricefish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii; Neopterygii; Teleostei; Euteleostei, Neoteleostei, Actinopterygii, Percomorpha, Acherinomorpha;
Beloniformes, Adrianichthyidae, Oryzinae, Oryzias.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.4%; Score 998; DB 2; Length 76
83.5%; Pred. No. 3.8e-53;
ive 20; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                    Liu R., Hong Y.,
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AX639947, AAT64312.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87566 MW; F5D01408748EC703 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer active octors of Go:0004871; F:signal transducer active octors octored oct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 765 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                    NCBI_TaxID=8090;
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Name=stat3;
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed E.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

MEDLINE-22388257; Medner E.S., Wadnefer C.F., Bhat N.K.,

MEDLINE-22388257; Medner E.S., Wadnefer C.F., Bhat N.K.,

MEDLINE-22388257; Medner E.S., Rubin G.M., Hong L.,

MEDLINE-22388257; Medner E.S., Rubin G.M., Hong L.,

MEDLINE-22388257; Medner E.S., Robin G.M., Medner E.S.,

MEDLINE-22388257; Medner E.S., Medner M.D., Medner M.D., Medner E.S.,

MEDLINE-22388257; Medner E.S., Garcia A.M., Gay L.J., Hulyk S.W.,

MEDLINE-22388257; Medner E.S., Retteman M., Madan A., Rodrigues S., Sanchez A.,

MILING M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Medriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

MEDLINE-22388257; Medner M.S., Medner M.S., Schnerch A., Schein J.E.,

Medner S.J., Marra M.A.,

Medner S.J., Marra M.A.,

Medner S.J., Marra M.A.,

Medner S.J., Medner M., Stalska U., Smailus D.E., Schnerch A., Schein J.E.,

Medner S.J., Marra M.A.,

Medner S.J., Medner M.A., Medner M. M., Medner M., M
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                                                                                                                                                                                                                                                                                       61 GNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                                                                                                                                                          2 HPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN 60
                                                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 785;
                                                                                                                                                                                                   16; Indels
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
BMBL, BC068120; AH68120.1; -.
ZFIN; ZDB-GENE-980526-68; stat3.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
                                                                                 785 AA; 89643 MW; 81F231BDE27DE938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                         85.4%; Score 998; DB 2;
83.5%; Pred. No. 3.9e-53;
                                                                                                                                                                                                20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last anno
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                   Matches 192; Conservative
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                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyprinidae; Dani
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=stat3;
                                                                                       SEQUENCE
                                                                                                                                           Query Match
                                                                                                                                                                            Best Local
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Q6NV46;
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     88 BB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 IACIGGPPNICLDRLETWITSLAESQLQIRQQIRKLEELQQKVSYKGDPIIQHRPALEEK 309
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Thesis (1998), University of Melbourne, Australia.

EMBL; Al005693; CAA06677.1; -.

REMBL; Al005693; CAA06677.1; -.

RESP: P42277; 18G1.

ZFIN; ZDB-GENE-980526-68; stat3.

R GO; GO:00004871; F:signal transducer activity; IEA.

GO; GO:0007700; F:transcription factor activity; IEA.

GO; GO:00074871; F:signal transducer activity; IEA.

GO; GO:00004871; F:signal transducer activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR00980; SH2.

R InterPro; IPR0017; STAT.

R Pfam; PF0017; STAT alpha; 1.

R Pfam; PF00107; STAT alpha; 1.

R Pfam; PF0265; STAT int; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 HPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDM-ODLN
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000242; P:intracellular signaling cascade; IEA.
GO; GO:000555; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000980; SH2.
InterPro; IPR000380; SH2.
InterPro; IPR001217; STAT.
Pfam; PF0017; STAT.
Pfam; PF01017; STAT_labha; 1.
Pfam; PF01017; STAT_labha; 1.
Pfam; PF02864; STAT_labha; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 IVDLFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVELFRNIMKSAFVVEROPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                        85.4%; Score 998; DB 2; Length 786;
83.5%; Pred. No. 3.9e-53;
live 21; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                          90039 MW; FC7371D0B0E5447E CRC64;
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92151 MW; 74BC4EA401C3C942 CRC64;
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Last sequence update)
Last annotation update)
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Pred. No. 4e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              806 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio)
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.5'
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                               PROSITE; PS50001; SH2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription factor.
                                                                                                                                                                                                                                                                                             786 AA;
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PROSITE; PS50001;
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60 NGNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 QIACIGGPPKICLDRLETWITSLGEIOLOIRQQIKKLEELQQKVSYKGDPIIQHRPALEE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDL
                                                                                                                                                                                                                                                                                       GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                              Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Wataryoza, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIVELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFATAVALLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 KIVDLFRNLMKSAFVVERQRCMPMHPDRPLVIKTGVQFTNKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Signal transducer and activator of transcription (Fragment)
Name=STAT3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Indels
                                                                                                                                                                                                                              Johnson M.C., Mourich D.V., Leong J.C.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U60333; AAB60926.1; --
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arredondo J.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.6e-51;
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ive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.5%; Score 964;
80.1%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR008967; PS3 like_DNA_bnd.
InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
                                                            Created)
                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta (Rhesus macaque).
                                                                      01-JUL-1997 (TrEMBLrel. 04, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15,
                                                            04,
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NCBI_TaxID=9544;
                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                         NCBI_TaxID=8022;
                                                                                                                   Name=rbtStat3;
                                                          01-JUL-1997
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                                           GNNQ-SVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
                                                                                                                                             IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                                                               189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                   HPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:00073700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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 5
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 Indels
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 15;
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82.2%; Pred. No. 1.1e-51;
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Mismatches
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Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
SMART; SMO0252; SH2; 1.
PROSITE; PS50001; SH2; 1.
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Matches 189; Conservative
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EMBL; AF227560; AAF73401.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VQKTLTDEELADWKRRQQIACIGGFPNICLDRLENWITSLAESQLQTRQQIKKLEELQQK 60
    HSSP; PA2277; 1867.

R HSSP; PA2277; 1867.

R GO; GO:0006871; F:signal transducer activity; IEA.

R GO; GO:0004871; F:signal transducer activity; IEA.

R GO; GO:000700; F:transcription factor activity; IEA.

R GO; GO:0007165; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:0007165; P:signal transduction; IEA.

R GO; GO:0007165; P:signal transduction; IEA.

R InterPro; IPR008267; FS3 1ike_DNA_bnd.

R Pfam; PF01017; STAT_alpha; 1.

R Pfam; PF01017; STAT_alpha; 1.

R Pfam; PF01017; STAT_bind; 1.

R NON TER 163 163

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R SEQUENCE 163 AA; 18855 WW; DD3F11E7F5B9878C CRC64;
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                                                                                                                                                                                                                                                                                      Ouery Match 54.7%; Score 639; DB 2; Length 163; Best Local Similarity 96.1%; Pred. No. 6.9e-32; Matches 123; Conservative 1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild type Leu substituted with Ala; corresponds to 148 position of Stat-3 protein"
213. .229
/note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is mouse Stat3 mutant (L148A) protein fragment containing 130-358 amino acids of Stat3 protein. This mutant is obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis; therapy; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids)
                                                                                                                                                                                                                                                                                                                                                Aaw03170 | Aaw62995 | Abu04747 | Abu04735 |
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AAY72847
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                                                                                                                                                May 25, 2005, 17:14:45 ; Search time 121.891 Seconds (without alignments) 726.619 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse
                                                                                                                                                                                                                                                                             1 NHPTAAVVTEKQQMLEQHAQ.....IKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aay72850
Aay72846
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Aar82993 H
Aab19964 H
                                                                                                                                                                                                                                                                                                                                                                                                                                    2105692
                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                     2105692 segs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                        OM protein - protein search, using sw model
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AAW03176
AAY72863
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AAB357164
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ADD44738
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geneseqp2003as:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
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//note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"
213. .229
//note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"
by replacing Leu 148 with Ala in Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, bNA binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                                                                                                                                                                      1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                        GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                       GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGILSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                               ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 1172; DB 4; Length 229; Best Local Similarity 100.0%; Pred. No. 1.2e-101; Matches 229; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse Stat3 protein fragment #8 (130-358 amino acids).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-2000; 2000WO-US023822
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                                                                                                                                                            Sequence 229 AA;
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                                                                                                                                                                                                                                                                                                                                                   1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription;
                                                                                                                                                                                                                                                                                                                                                                                         61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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/note= "Stat3-c-Jun interaction region 2;
342-358 position of Stat3 protein"
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                                                                                                                                                                                                                                                                                              1; Indels
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/note= "Stat3-c-Jun interaction re
130-154 position of Stat3 protein"
                                                                                                                                                                                                                                                              Score 1167; DB 4;
Pred. No. 3.5e-101;
0; Mismatches 1;
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            Claim 65; Page 76-77; 86pp; English.
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                                                                                                                                                                                                                                                               99.6%;
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                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                  Sequence 229 AA;
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27-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                   GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGILSAMEYVQKTLTDEELADWKRRPEI 143
                                                                                                                                                                                                                                                                                                                                                                                                                   121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                          The present sequence is mouse Stat3 protein fragment containing 107-358 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of typroliferative diseases and also for treating cancer and psoriaeis. A Stat protein comprises the N-terminal domain, colled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                             83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                  NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                 236. .252
/note= "Stat3-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                     1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Stat3-c-Jun interaction region 1; corresponds 130-154 position of Stat3 protein"
                                                                                                                                                                                                                                                                                             Gaps
                                   Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 252
                                                                                                                                                                                                                                                                   99.6%; Score 1167; DB 4; Length 252; 99.6%; Pred. No. 4e-101; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse Stat3 protein fragment #2 (107-377 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                      Claim 65; Page 73; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY72841 standard; protein; 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-2000; 2000WO-US023822,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                               Best Local Similarity 99.6
Matches 228; Conservative
           WPI; 2001-226705/23.
                                                                                                                                                                                                                                             Sequence 252 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204
                                                                                                                                                                                                                                                                     Query Match
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61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is mouse Stat3 protein fragment containing 107-377 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of Stat protein comprises and also for transcription e.g., cellular Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 NEPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDEPFNYKTLKSGGDMODLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                     Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.6%; Score 1167; DB 4; Length 271; 99.6%; Pred. No. 4.4e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Darnell JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                          Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                              Claim 65; Page 67-68; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR72082 standard; protein; 770 AA.
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93US-00126595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 99.6
Matches 228; Conservative
(UYRQ ) UNIV ROCKEFELLER
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                                                                          Zhang X, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse Stat3 (19sf6).
                                                                                                                                              WPI; 2001-226705/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 271 AA;
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ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
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/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"
                                                                                                                                                                                                                                    - useful for diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                       STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from ligand-activated receptor kinase complexes followed by nuclear translocation and DNA binding to activate transcription. Recombinant STAT4 can be obtd. using cDNA clone 19sf6 (AAT31278) obtd. from splenic/thymic cells. STAT4 includes a DNA-binding domain (see also AAW03167) capable of both receptor recognition and message delivery vi DNA binding in a receptor-ligand specific manner. STAT proteins and that antagonists used to inhibit STAT-mediated signal transduction and activation of transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GINIQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNNOSVIRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                         signal transducer and activator of transcription (STAT) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VELFRNIAKSAFVVERQPCMPM4PDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                                    New STAT protein DNA-binding domain peptide(s) - useful for di
preventing or treating cellular dysfunction, e.g. oncogenesis,
inflammation, parasitic disease or autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VELFRNIMKSAFVVEROPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.6%; Score 1167; DB 2; 99.6%; Pred. No. 1.8e-100; iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                  Disclosure; Page 87-90; 138pp; English.
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                                                                                                                                    Horvath CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY72863 standard; protein; 229
                    95WO-US017025
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                                                                                                (UYRO ) UNIV ROCKEFELLER
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                                                                                                                                                                           WPI; 1996-333941/33.
N-PSDB; AAT31280.
                                                                                                                                      Wen Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 770 AA;
                    28-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                      Darnell JE,
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Region
                                                                                                                                                                                                                                                                                                                                                           Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
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                                                                                                                                                                                                                                                                                                            A fragment encoding the human Stat91 protein was used to screen a murine thymus and splean cDNA for homologous proteins. A highly homologous gene (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080) (Stat1) that was responsive to interferon-gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AAQ89339 + Ceptor recognition factor proteins were isolated. The 2 genes (AAQ89339 + 1381 and 138f1 and 138f6 and encoded proteins termed stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                  2;
                                                                                                Zhong
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Pred. No. 1.8e-100;
0; Mismatches 1;
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/label= DNA binding_domain
/note= "Claim 3, page 110"
                                                                                                    Wen
                                                                                                                                                                                                                                                                             Claim 1; Page 107-110; 160pp; English.
                                                                                                  Shuai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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94US-00212184.
94US-00212185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.68;
                                                                                                Schindler CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.6
Matches 228; Conservative
                                                           ROCKEFELLER
                                                                                                                                        1995-139598/18.
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                                                                                                                                                         N-PSDB; AAQ89340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STAT; STAT4;
DNA binding p
                                                         (UYRQ ) UNIV
11-MAR-1994;
11-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9620954-A2
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                                                                                                Darnell JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse STAT4
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Key Domain Mus

RESULT 6 AAW03176

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        /note= "Wild type Val substituted with Ala corresponds to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPWLEERI 180
                                                                                                                                                                                                                                                                                                               containing 130-358 amino acids of Stati protein. This mutant is obtained by replacing Val 151 with Ala in Stati protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying speirs which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                              213. 7.229
/note= "Stat3-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GINIQSVTRQKAQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                              Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                      present sequence is mouse Stat3 mutant (V151A) protein fragment
                                                                                                                                                                                                                                             Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.2%; Score 1163; DB 4; Length 229; 99.1%; Pred. No. 8.3e-101; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VELFRNLMKSAFVVERQPCMPWHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                  Darnell JE;
                                                                                                                                                                                                Wrzeszcynska MH,
                                                                                                                                                                                                                                                                               Claim 66; Page 86; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE22055 standard; protein; 720
                                                                                                                           30-AUG-2000; 2000WO-US023822
                                                                                                                                                  99US-00387418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.1
Matches 227; Conservative
                                                                                                                                                                         (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Stat3beta protein.
                                                                                                                                                                                                Shang X, Horvath C,
                                                                                                                                                                                                                        WPI; 2001-226705/23
Misc-difference 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 229 AA;
                                                                              WO200116605-A2
                                                                                                                                                  31-AUG-1999;
                                                                                                    08-MAR-2001.
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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, tissue ischaemia in the lower extremities, infarction, suffocation, shock, offoroic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, cpilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus erythematosus, multiple scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary bilary cirrhosis, pernicious anaemia, autoimmune hyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      idiopathic thrombocycopenia purpura, Grave's disease, Goodpasture's disease, theumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human
hypoxia, stroke, angiogenesis, myocardial infarction, hypoglycaemia; inflammation, chronic obstructive pulmonary disease, cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; soleroderma; shock, chronic artive hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility, anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disease; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion; Statbeta.
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Pred. No. 1.8e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 713. .714
/note= "Encoded by ACA CCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dalton W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-2001; 2001WO-US028254.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYSF-) UNIV JOHNS HOPKINS.
(UYSF-) UNIV SOUTH FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-362218/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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Length 769;

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conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vascopastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB573702 to ABB57374) or by determining the protein sequences in ABB573702 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition.improving drugs or indicator when screening diseases. ABB199913 and AB199914 represent primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
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                                                                       NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN
                                                                                                                                ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                   1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                           GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                    ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Examining the ischemic condition (e.g. occlusive ischemia) by measurexpression levels of particular genes defined in the specification of determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for examining ischaemic conditions, comprising measuring the average.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse ischaemic condition related protein sequence SEQ ID NO:398.
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                                                                                                                                                                                                                                                                                  VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease
Indels
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 1084-1087; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             ABB57164 standard; protein; 769
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 Conservative
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Sequence 769 AA;

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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
                                                                                              30 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                    immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.
                                                                                                                                                                                                 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                  GNNOSVTROKMOOLEQMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEBLADWKRRPEI
                                                                                                                                                                  190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
                                 Gaps
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                                                                                                                                                                                                                                                                                   VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                                                                     VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; signal transducer and activator of transcription
Score 1156; DB 5;
Pred. No. 1.9e-99;
                 Pred. No. 1.96
1; Mismatches
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   98.6%;
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FLORIDA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-362218/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Stat3 protein.
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                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yu H, Pardoll D,
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                 Local Simi.
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     Query Match
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Matches
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tiseue ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tiseua ischaemia in the lower extremities, infarction, trauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglyaemia, children adult respiratory distress syndrome, cardiac arrest, nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus erythematosus, multiple sclerosis, insulin dependent diabetes mellitus, circhematosus, multiple sclerosis, insulin dependent diabetes mellitus, sysparen's syndrome, scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary circhosis, pernicious maemia, autoimmune thyroiditis, idiopathic Addison's disease, viciligo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, coodpasture's disease, rheumatoid arthritis, circhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disease which includes sarcomas and carcinoma, liposarcoma, degenerative diseorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The present sequence is human Stat3 \$X\$

Sequence 769 AA;

ö 120 249 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN GNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI Gaps .; 0 98.6%; Score 1156; DB 5; Length 769; 98.7%; Pred. No. 1.9e-99; 2; Indels 1; Mismatches Matches 226; Conservative Best Local Similarity 61 Query Match a ò ò

VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229 310 VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358 181 ઠે 셤

180

121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI

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AAE22056 standard; protein; 769 AA. AAE22056; RESULT 11

25-JUL-2002 (first entry)

Human protein related to angiogenesis regulation.

Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; spilepsy; polymyositis; theumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; disored si disease; ulcerative colitis; sarcona; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.

Homo sapiens

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Control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                               Modulating anglogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 83-85; 94pp; English.
                                                                                                                                                                                                                                                                                                          Dalton W;
                                                                                                                                                                  08-SEP-2000; 2000US-0231212P
                                                                                                        10-SEP-2001; 2001WO-US028254
                                                                                                                                                                                                                                                                                                          Jove R,
                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-362218/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of transcription 3.
                                                                                                                                                                                                                   UNIV JOHNS
UNIV SOUTH
                                                                                                                                                                                                                                                                                                       Yu H, Pardoll D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 769 AA;
WO200220032-A1.
                                                    14-MAR-2002.
                                                                                                                                                                                                                   (UYJO) (UYSF-)
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Gaps ö 98.6%; Score 1156; DB 5; Length 769; 2; Indels Pred. No. 1.9e-99; 1; Mismatches 2 98.78; Matches 226; Conservative Best Local Similarity Query Match

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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189 190 GNNQSVTRQXMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI 61 GNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI

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1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDMQDLN 60

121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180

181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229

310 VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLJVKFPEL 358

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Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6; intracellular transcription factor; interleukin-6; medicament; variant; pharmaceutical; autoimmune disease; inflammatory; human.
                                                                                                                                                                                                                                                                                                                                                                     New human Signal Transducer and Activator of Transcription 3 (STAT3) allelic variant useful for treatment of autoimmune and inflammatory
                                                                                                                                                                                                                                                                               (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
                                                                                                                                                                                                                                                                                                          Della Pietra L;
AAY03768 standard; protein; 770 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 9-13; 32pp; English.
                                                                                                                                                                                                                                                        97EP-00116061
                                                                          Human STAT3 allelic variant
                                                  (first entry)
                                                                                                                                                                                                                                                                                                           Serlupi-Crescenzi O,
                                                                                                                                                                                                                                                                                                                                    WPI; 1999-192664/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX29281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 770 AA;
                                                                                                                                                                                                                               18-FEB-1998;
                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                        16-SEP-1997;
                                                  11-JUN-1999
                                                                                                                                                                                                      31-MAR-1999
                                                                                                                                                                              EP905234-A2
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                                                                                                                                                                                                                                                                                                                                                                                                    disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a mouse acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (IL-6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA library using a polymerase chain reaction product (amplified using primers derived from an IL-6-treated mouse liver peptide) as a probe. AFRF-inhibitors, e.g. antibodies, antisense oligonucleotides or ribozymes, may be used to treat diseases induced by IL-6, e.g. inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309
                                                                                                                                         Mouse; acute phase response factor; transcription factor; interleukin-6; signal transmission; liver; antibody; antisense; ribozyme; antiinflammatory; antitumor; hypotensive; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                             New acute phase response factor - for developing inhibitory agents for treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NHPTAAVVTEKOOMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.6%; Score 1156; DB 2; Length 770; 98.7%; Pred. No. 1.9e-99; ive 1; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                  Mouse liver acute phase response factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page 20-22; 31pp; English.
                                      standard; protein; 770 AA.
                                                                                                                                                                                                                                                                      95EP-00104670
                                                                                                                                                                                                                                                                                               94JP-00065825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.7'
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                   Kishimoto T;
                                                                                                                                                                                                                                                                                                                        (KISH/) KISHIMOTO T.
                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-346089/45.
                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT05619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 770 AA;
                                                                                                                                                                                                                                                                                                04-APR-1994;
                                                                                                                                                                                                                                                                       29-MAR-1995;
                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                      EP676469-A2.
                                                                                                                                                                                                                                              11-0CT-1995
                                                               AAR82995;
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                                       AAR82995
               RESULT 12
                             AAR82995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 NHPTAAVVTEKQOMLEQHLQDVRKRVQDLEQKNKVVENLQDDFDFNYKTLKSQGDMQDLN 189
The present sequence represents a predominant allelic variant of human Signal Transducer and Activator of Transcription 3 (STAT3) protein, an intracellular transcription factor which mediates IL-6 signals. The encoding sequence differs from the original published human STAT3 gene sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3 protein can be used for the recombinant expression of the variant. STAT3 protein is useful as a medicament or pharmaceutical composition for treatment of autoimmune or inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                          98.6%; Score 1156; DB 2;
98.7%; Pred. No. 1.9e-99;
iive 1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 226; Conservative
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RESULT 13

229

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Signal transducer and activator of transcription; STAT3; drug development; drug discovery; crystal; inflammation; allergy; asthma; leukaemia; anaemia; neutropaenia; thrombocytopaenia; cancer; obesity;
                                       250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPWLEERI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Conserved N-terminal domain of the STAT family"
                                                                                                   VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKPPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying compounds that bind to signal transducer transcription proteins, useful for the production of
                                                                                                                                                                                                                                                                                                                                                                           viral disease; growth retardation; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Darnell JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                             AAE14652 standard; protein; 770 AA
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                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vinkemeier U, Moarefi I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                             Murine STAT3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-033337/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6312887-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JAN-1998;
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                                                                                                                                                                                                                              AAE14652;
                     121
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Domain
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                                                                                                                                                                                 AAE14652
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                                                                                                          셤
                                                                                                                                                                                                               The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater than S.O Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New crystals of an N-terminal fragment of a signal transducer and activator of transcription that effectively diffracts x-rays, useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                               transducer and activator of transcription; crystal;
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                                                                                                                                                                                                                       19. .21
/label= 3(10) helix of alpha helix 2
28. .33
/label= Alpha helix 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kuriyan J;
                               N-terminal domain of murine STAT-3 protein.
                                                                                                                                                                                                                                                                                     35. .40
/label= Alpha helix 4
43. .47
/label= Alpha helix 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Darnell JE,
                                                                                                                                                                                                          'label= Alpha helix 2
                                                                                                                                                                 . .9
label≂ Alpha helix 1
                                                                                                                                                                                                                                                                                                                                                                    /label= Alpha helix 6
77. .96
/label= Alpha helix 7
                                                                                                                                                                                                                                                                                                                                                                                                                      99. .119
/label= Alpha helix 8
                                                                                                                                             location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug screening and development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-00012710.
08-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moarefi I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 98.77
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYRQ ) UNIV ROCKEFELLER.
                                                             STAT; signal transdu
drug design; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-505108/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-1998;
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                                                                                                                                             Key
Region
                                                                                                             Mus sp
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The invention relates to methods for detecting compounds that bind to signal transducer and activator of transcription (STAT) proteins for the discovery and development of new drug compounds based on the structural properties of the protein crystal. The methods include: identifying a compound that binds to the N-terminal domain of a STAT protein.

If identifying a compound that enhances or diminishes the binding of the dimeric STAT proteins to each other and/or their nucleic acid binding site, or identifying a compound that enhances or diminishes the ability of STAT protein dimers to induce the expression of a gene operably under the control of a promoter concaining at least two adjacent weak binding sites for STAT protein dimers. The methods are used for identifying new drugs. An antagonist of STAT verminal dimeric interactions that inhibits the binding of the STAT dimers to adjacent weak binding sites on a promoter of a gene, could be useful as drugs in the treatment of diseases, e.g. inflammation, allergy, asthma and leukamias. On the other hand, an agonist of N-terminal dimeric interactions between STAT dimers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      can be used as drugs in the treatment of diseases e.g. anaemia, neutropaenia, thrombocytopaenia, cancer, obesity, viral diseases and growth retardation. The present sequence is murine STAT3 protein
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Example, Col 47-50; 44pp; English.
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and activator of new drugs.

Kuriyan J;

Search completed: May 25, 2005, 17:36:38 Job time : 123.057 secs

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Sequence 18, Application US/09387418A
Sequence 18, Application US/09387418A
Patent No. 6391572
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
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Sequence 14,
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Sequence 3
Sequence 5
Sequence 5
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Sequence 3
Sequence 9
Sequence 8
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Sequence 5
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/cgn2_6/ptcdata/1/iaa/6A_COWB.pep:*
/cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/PcTUS_COMB.pep:*
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Compugen Ltd.
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US-09-387-418A-19
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US-08-369-796-12
US-08-852-091-12
US-08-956-652-12
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US-08-956-652-12
US-08-956-652-12
US-09-364-970-3
US-09-364-970-5
US-09-364-970-5
US-09-364-970-5
US-09-364-970-5
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US-09-387-418A-31
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US-09-556-273-8
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US-08-276-099A-14
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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
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Perfect score:
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Maximum DB
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No.
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Sequence 30, Application US/09387418A

Patent No. 631572

GRNERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Mrzeszczynaka, Melissa H
APPLICANT: Darnell Jr., James E
ITILE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-23
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 1e-97;
0; Mismatches 0; Indels
        US-09-387-418A-29
US-09-387-418A-19
US-09-387-418A-15
US-09-387-418A-23
US-09-387-418A-16
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US-09-387-418A-17
US-09-387-418A-17
US-09-387-418A-17
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US-08-356-65-6
US-08-356-65-6
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US-08-956-653A-6
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Best Local Similarity 100.
Matches 229; Conservative
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ORGANISM: Mus musculus
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11150
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Sequence 14, Application US/09387418A

Sequence 14, Application US/09387418A

Patent No. 6391572

GENERAL INFORMATION:
APPLICANT: Wizesczynska, Melissa H
APPLICANT: 1990-08-31

CURRENT APPLICATION NUMBER: US/09/387,418A

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 3.6e-97;
                                                                                                                                                   181 VELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVQ
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APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wzeaczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
TITLE OF INVENTION: METHODS FOR IDENTIFYING
ITILE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 99.6%;
Matches 228; Conservative (
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; ORGANISM: Mus musculus
US-09-387-418A-9
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Best Local Similarity
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US-09-387-418A-14
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us-10-09

...c_uLCANT: Darnell Ur., James E

; TILLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: 0599/387,418A
; CURRENT FILING DAIR: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
SEQ ID NO 18
LENGTH. ...
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Sequence 28, Application US/09387418A
Sequence 28, Application US/09387418A
Sequence 28, Application US/09387418A
GENERAL INFORMATION:
APPLICANT: Applicant: Alanga H
APPLICANT: Wizeaczynska, Melissa H
APPLICANT: Darnell Jr., James E
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: MITERACTIONS
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-23
CURRENT APPLICATION VUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
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Pred. No. 2.9e-97;
0; Mismatches 1; Indels
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99.6%; Score 1167; DB 3;
Best Local Similarity 99.6%; Pred. No. 2.9e-97;
Matches 228; Conservative '0; Mismatches 1;
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Best Local Similarity 99.6%;
Matches 228; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-387-418A-28
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Sequence 12, Application US/08852091
Patent No. 588328
GENERAL INFORMATION:
APPLICANT: 210ng Wen
APPLICANT: Zhong Wen
TITLE OF INVENTION: FRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
ITILE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 NHPTAAVVTEKQOMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                 250 ACIGGPPNICLDRLENWITSLABSQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                           121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                                          181 VELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLVKFPEL 229
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Pred. No. 1.4e-96;
0; Mismatches 1;
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APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-NAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 08369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 Hackensack Avenue
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-852-091-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                 RESULT 7
US-08-852-091-12
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Patent No. 5716622

GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Curt M. Horvath
APPLICANT: Zhong Wen
APPLICANT: Though Wen
APPLICANT: The OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
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                                                                                                                                                  84 GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                         1 NHPTAAVVTEKOOMLEOHAODVRKRVODLEOKMKVVENLODDFDFDFNYKTLKSOGDMODLN
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  Gaps
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Pred. No. 1.4e-96;
0; Mismatches 1; Indels
  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 411 Hackensack Avenue
CITY: Hackensack
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ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 99.6
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  Conservative
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COUNTRY: USA
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                                                                                                                        61
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Matches
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61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                    Sequence 12, Application US/08820754
Fatent No. 5976835
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.6%; Score 1167; DB 2; Length 770; 99.6%; Pred. No. 1.4e-96; tive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US.

ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA::
INTERPRETATION DATA:
PILING DATE: 19-MAR-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1997
PRIOR APPLICATION NUMBER: US 07/980,498
FILING DATE: 13-MAR-1992
PRIOR APPLICATION NUMBER: US 07/984,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: 20-1993
PRIOR APPLICATION NUMBER: 20-1993
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION NUMBER: 26-742
PRIOR APPLICATION NUMBER: 26-742
PRIOR APPLICATION NUMBER: 26-742
TELEPONEY/AGENT INFORMATION:
TELEPANEY 201 343-1684
TELEPANEY 201 343-1684
TELEPANEY 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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LENGTH: 770 amino acids
TYPE: amino acid
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Best Local Similarity 99.6
Matches 228; Conservative
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121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                        250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
190 GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEXVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INCORNATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
ITILE OF INVENTION: BECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.6%; Score 1167; DB 3; Length 770;
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION NUMBER: US 07/864,296
FILING DATE: 19-MAR-1994
APPLICATION NUMBER: WO US 97/854,296
FILING BATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: WO US 93/02569
FILING BATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 19-MAR-1993
ATTONEY/AGENT INFORMATION:
ANDELS ALS SERVICED TO SER
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 12, Application US/08956652; Patent No. 6013475
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 770 amino acids
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amino acid
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STATE: New Jersey
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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                                     Length 770;
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Patent No. 6124118
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Pu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES: 25
                                                                                                                                                                              1; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
                                                                                                                     Query Match
99.6%; Score 1167; DB 3;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1;
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rer: 600-1-073 CIP
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CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
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FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPOTTER: IBM PC COMPALIBLE
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                                 ; MOLECULE TYPE: protein US-08-956-869-12
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ADDRESSEE: Klauber &
STREET: 411 Hackensa
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US-08-948-547-12
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                                                                                                                                             130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                       61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                       250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                                          1 NHPTAAVVTEKOOMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                      121 ACIGGPPNICLDRLENWITSLAESOLOTROOIKKLEELOOKVSYKGDPIVOHRPMLEERI
                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Schindler, Christian W. APPLICANT: Schindler, Christian W. APPLICANT: Schindler, Christian W. APPLICANT: Pu, Xian-Yuan APPLICANT: Wen, Zilong APPLICANT: Weng, Zhong TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
Best Local Similarity 99.6%; Pred. No. 1.4e-96; Matches 228; Conservative 0; Mismatches 1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR-1992
RIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,869
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/212,185
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08956869
Patent No. 6030808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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US-08-956-869-12
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                        US-09-364-970-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
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Batent No. 6235873

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR

TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING

FILE REFERENCE: 600-1-222

CURRENT APPLICATION NUMBER: US/09/364,970

CURRENT FILING DATE: 1999-07-31

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                            NHPTAAVVTEKOOMLEOHAODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN
                                                                                                                                                                                                                                                                                                                                                                                                           190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGILSAMEYVQKTLTDEELADWKRRPET
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                                                                                                                                                                                                                 Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                               99.6%; Score 1167; DB 3;
99.6%; Pred. No. 1.4e-96;
live 0; Mismatches 1;
                                    TELEX: 133521
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
  : 201 487-5800
201 343-1684
                                                                                                                                                                                                             Query Match
Best Local Similarity 99.6
Matches 228; Conservative
                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-948-547-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mus musculus
TELEPHONE:
                      TELEFAX:
TELEX: 1
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US-09-364-970-3
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Sequence 5, Application US/09364970

Patent No. 6235873

GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSITTUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULAFORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: USES FOR IDENTIFYING MODULAFORS OF ACTIVITY INCLUDING
FILE REFERENCE: 600-1-252
CURRENT FALING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE PATENTIAL OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 GNNQSVIRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Pu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECCONITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.6%; Score 1167; DB 3;
99.6%; Pred. No. 1.4e-96;
iive 0; Mismatches 1;
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APPLICATION NUMBER: US/08/956,653A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 12, Application US/08956653A; Patent No. 6338949; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.6
Matches 228; Conservative
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CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-5
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NHPTAAVVTEKOOMLEQHAODVRKRVODLEQKMKVVENLODDFDFNYKTLKSQGDMQDLN
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Patent No. 6605442

GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Wen, Zilong
ITILE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
ITILE OF INVENTION: SEQUENCES: ADDRESSE: ALAUBER of SEQUENCES: SCORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: All Hackensack
COUNTRY: USA

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:
COMPUTER: IBW PC Compatible
COMPUTER: IBW PC Compatible
COMPUTER: IBW PC Compatible
COMPUTER: IBW PC Compatible
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.6%; Score 1167; DB 3; Length 770;
99.6%; Pred. No. 1.4e-96; .
Live 0; Mismatches 1; Indels
                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 24-SEP-1993
ATTORNEY, AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
RECECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 770 amino acids
amino acid
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Best Local Similarity 99.6#
Matches 228; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-956-653A-12
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US-08-212-185-12
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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
  APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-MOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
UMBER: US/08/212,185
11-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acide TOPOLOGY: 1
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Search completed: May 25, 2005, 17:47:40 Job time: 29.6534 secs

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May 25, 2005, 17:36:58 ; Search time 100.287 Seconds '
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763.830 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:

SUMMARIES

	Description	Sequence 30, Appl	18,	Sequence 28, Appl	Sequence 14, Appl	Sequence 9, Appli	12	Sequence 12, Appl	Sequence 31, Appl	4	Sequence 2, Appli	'n	8	Sequence 56, Appl
	QI.	US-10-090-185-30	US-10-090-185-18	US-10-090-185-28	US-10-090-185-14	US-10-090-185-9	US-09-876-773-12	US-10-639-617-12	US-10-090-185-31	US-10-380-020-4	US-10-380-020-2	US-10-380-020-5	US-10-045-792-8	US-10-038-010-56
		13	13	13	13	13	11	11	13	15	15	15	14	14
	Query Match Length DB	229	229	229	252	271	770	770	229	720	769	769	770	770
do	Query Match	100.0	99.6	99.6	99.6	99.6	9.66	99.6	99.2	98.6	98.6	98.6	98.6	98.6
	Score	1172	1167	1167	1167	1167	1167	1167	1163	1156	1156	1156	1156	1156
	Result No.	-	7	m	4	S	9	7	80	σ	10	11	12	13

2, A 780, 380, 349,	Sequence 19, Appl Sequence 19, Appl Sequence 15, Appl Sequence 22, Appl Sequence 13, Appl Sequence 15, Appl	4, 17, 12, 12, 12, 12, 12, 12, 12, 12, 12, 12	Sequence 2, Appli Sequence 6, Appli Sequence 5, Appli Sequence 2, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	352, 823, 119, 44, A 550, 550, 8, Ap
US-10-117-087 US-09-925-302- US-09-925-302 US-10-116-275 US-10-116-275	13 US-10-090-185-29 13 US-10-090-185-19 13 US-10-090-185-12 13 US-10-090-185-23 13 US-10-090-185-23 13 US-10-090-185-13	13 US-10-090-185-20 13 US-10-090-185-17 9 US-09-833-205-4 13 US-10-090-185-12 14 US-10-245-120-3	US-10-245-120 US-10-245-120 US-10-639-617 US-09-833-205- US-09-876-773 US-10-245-120 US-10-308-279	16 US-10-75-889-152 17 US-10-492-043-19 17 US-10-639-617-4 18 US-10-925-297-550 19 US-09-185-24 19 US-09-833-205-6 11 US-09-876-773-8
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ALIGNMENTS

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APPLICANT: Zhang, Xiaokui
APPLICANT: Thang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION INMERS: US/10/090,185
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.0
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US-10-090-185-30; Sequence 30, Application US/10090185; Publication No. US20020197647A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Mus musculus
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LENGTH: 229
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US-10-090-185-14

Sequence 14, Application US/10090185

Sequence 14, Application US/10090185

Sequence 14, Application US/20020197647A1

Sequence 14, Application No. US20020197647A1

Septimize 1 INFORMATION:

APPLICANT: Wrzeszczynska, Melissa H

APPLICANT: Horvath, Curt M

APPLICANT: Horvath, Curt M

APPLICANT: Darnell Jr., James E

TITLE OF INVENTION: INTERACTIONS

FILE REFERENCE: 600-1-253

CURRENT APPLICATION NUMBER: 105/090,185

CURRENT APPLICATION NUMBER: 09/387,418

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTION OF 2.00

SED ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                           61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSBLAGLLSAMEYVQKTLTDEBLADWKRRPEI 120
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                                                                                                                                   Score 1167; DB 13; Length 229;
Pred. No. 6.4e-95;
0; Mismatches 1; Indels 0
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99.6%; Pred. No. 7.2e-95;
cive 0; Mismatches 1; Indels 0
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Matches 228; Conservative
                                                                                                                                                                                                           Matches 228; Conservative
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; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-14
TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                   Query Match
Best Local Similarity
                                                                   US-10-090-185-28
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APPLICANT: Zhang, Xiaokui
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Wizeszcz
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APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska,
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: NETHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR ITILE OF INVENTION: INTERACTIONS
FILE REPERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT APPLICATION NUMBER: 09/387,418
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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                                121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
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Pred. No. 6.4e-95;
0; Mismatches 1; Indels 0
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; Sequence 28, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/10090185
Publication No. US20020197647A1
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Best Local Similarity 99.6%;
Matches 228; Conservative 0
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130 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN 189
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INVENTION: RECEPTOR RECOGNITION FACTORS,
                       FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-58P-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 11;
3e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.6%; Score 1167; D
99.6%; Pred. No. 3e-9
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Darnell Jr., James E. Schindler, Christian Fu, Xian-Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/10639617
Publication No. US20050079543A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEO ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Klauber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wen, Zilong
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.6
Matches 228; Conservative
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                                                                  APPLICANT: Zhang, Xiaokui
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Userath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION NUMBER: US/10/090,185
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.6%; Score 1167; DB 13; Length 271; 99.6%; Pred. No. 7.9e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhong, Zhong
TITLE OF INVENTION: RECREPTOR RECOGNITION FACTORS, PROTEIL
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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COMPUTER: 1BM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09876773
Publication No. US200040058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
Wen, Zilong
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ADDRESSEE: Klauber & Jackson
Sequence 9, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackensack
STATE: New Jersey
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Best Local Similarity 99.6
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus US-10-090-185-9
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US-09-876-773-12
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Sequence 4, Application US/10380020
| Sequence 4, Application US/10380020
| Publication No US20040052762A1
| GENERAL INFORMATION:
| APPLICANT: Pardoll, Drew
| APPLICANT: Dove, Richard
| APPLICANT: Dalton, Willian
| TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
| CURRENT APPLICATION NUMBER: US/10/380,020
| CURRENT FILING DATE: 2003-03-07
| PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                         61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                          1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                 Gaps
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                                                                                   Length 229;
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                                                                                                                               Indels
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Pred. No. 2.6e-93;
1; Mismatches 2;
                                                                                 Score 1163; DB 13;
Pred. No. 1.4e-94;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-10-380-020-2
Sequence 2, Application US/10380020
; Publication No. US20040052762A1
                                                                                 99.2%;
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SOFWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 98.6%;
Best Local Similarity 98.7%;
Matches 226; Conservative
                                                                                      Query Match
Best Local Similarity 99.1
Matches 227; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo Sapiens
                        musculus
                      ; ORGANISM: Mus
US-10-090-185-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-380-020-4
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    TYPE: PRT
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Publication No. US20020197647A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alang, Xiaokui
APPLICANT: Wiresaczynaka, Melissa H
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 2002-03-04
PRIOR PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 GNNQSVTRQKWQQLEQWLTALDQWRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 99.6%; Score 1167; DB 17; Similarity 99.6%; Pred. No. 3e-94; 28; Conservative 0; Mismatches 1;
                                                                                                      APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-MOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
APPLICATION NUMBER: US 08/126,588
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/639,617
FILING DATE: 12-Aug-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 201 487-5800
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TELEX: 133521
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Best Local Similarity 99.67
Matches 228; Conservative
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250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
    190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI 249
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                                                 121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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                                                                                                                                                                                                                                                                                                                                                                                          Moarefi, Ismail
Darnell, Jr., James B.
Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A STAT PROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                310 VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                    181 VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1156; DB 14;
Pred. No. 2.9e-93;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-Oct-2001
. CLASSIPICATION: CURNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO SEQUENCE DESCRIPTION: SEQ ID NO: US-10-045-792-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                            Sequence 8, Application US/10045792
Publication No. US20030003563A1
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
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COUNTRY: USA
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Best Local Similarity 98.7°
Matches 226; Conservative
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APPLICANT: Pardoll, Drew
APPLICANT: Fardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: 05/10/10/20
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 769
                                                           APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
CURRENT PILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNNOSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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98.7%; Pred. No. 2.8e-93.
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1; Mismatches
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                                                                                                                                                                                                                                                                    SOFTWARE: Patentin version 3.0 SEQ ID NO 2 LENGTH: 769
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.7
Matches 226; Conservative
                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo Sapiens
US-10-380-020-2
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GENERAL INFORMATION
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                                          APPLICANT:
APPLICANT:
APPLICANT:
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Gaps

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Length 770;

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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKWKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                       1 NHPTAAVVTEKOOMLEOHAODVRKRVODLEOKMKVVENLODDFDFNYKTLKSQGDMQDLN
                                                       Query Match 98.6%; Score 1156; DB 14; Best Local Similarity 98.7%; Pred. No. 2.9e-93; Matches 226; Conservative 1; Mismatches 2;
; ORGANISM: Human
US-10-117-087-2
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US-09-925-302-780
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                      130 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN 189
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                                                                                                                                                                                                     Sequence 56, Application US/10038010
Fublication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: HYBRIGENICS
TILE REPERENCE: B4767A
CURRENT PILING DATE: 2002-07-23
FRICH REPERIOR DATE: 2002-07-23
FRICH REPERIOR DATE: 2001-02
NUMBER OF SEQ ID NOS: 67
SUMMER OF SEQ ID NOS: 67
SUMMER OF SEQ ID NOS: 67
SUMMER OF SEQ ID NOS: 67
SEQ ID NO 56
LENGTH: 770
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Pred. No. 2.9e-93;
1; Mismatches 2; Indels 0
                                                                         181 VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
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Publication No. US20030166854A1

GENERAL INFORMATION:
APPLICANT: SERLUP-CRESCENZI, Ottaviano
APPLICANT: BELLA PIETRA, Linda
TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
FILE REFRERENCE: SERLUPI=2
CURRENT APPLICATION NUMBER: US/10/117,087
CURRENT PILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US/09/526,542
PRIOR FILING DATE: 2000-03-19
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: STAT3 : Transcription factor to LOCATION: (1)..(770)
CTHER INFORMATION:
US-10-038-010-56
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Best Local Similarity 98.7
Matches 226; Conservative
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250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
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                                190 GNNQSVTRQKOQQLEQMLTALDQMRRSIVSELAGILSAMEYVQKTLTDEELADWKRRQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGILSAMEYVQKTLTDEELADWKRRQQI
GNNQSVTROKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                     121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 780, Application US/09925302
| Sequence 780, Application US/09925302
| Patent No. US20020044941A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REPRENCE: PA104
| CURRENT APPLICATION NUMBER: US/09/925,302
| CURRENT FILING DATE: 2001-08-10
| PRIOR APPLICATION NUMBER: PCT/US00/05918
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-12
| WUMBER OF SEQ ID NOS: 8966
| SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 793;
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Pred. No. 3e-93;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: May 25, 2005, 18:21:54
Job time : 101.62 secs
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Best Local Similarity 98.7
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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SEQ ID NO 2 LENGTH: 770 TYPE: PRT

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 25, 2005, 17:24:07 ; Search time 21.6038 Seconds (without alignments) 1019.898 Million cell updates/sec

US-10-090-185-30 1172 1 NHPTAAVVTEKQOMLEQHAQ.....IKTGVQFTTKVRLLVKFPEL 229 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	ISGF3 p91-related	DNA-binding protei	interferon-depende	gamma-interferon a	interferon alpha-i	mammary gland fact	mammary gland fact	transcription acti	mammary gland fact	interleukin-4-indu	conserved hypothet	DNA-Binding Protei	tpr protein - huma	hypothetical prote		chromosome segrega	hypothetical prote	epimorphin - mouse	microtubule bindin	myosin heavy chain	myosin heavy chain	364K Golgi complex	hypothetical coile	dystrophin, muscle	kinesin-related pr	coiled coil protei	median body protei	MSP-300 protein -	epidermal growth f
SUMMAKIES	10	I49508	A5444	A46159	A56047	A46160	149274	S54772	G02317	855527	A54740	A70387	157557	833124	G72593	T27075	AE1947	T24806	S51193	T13030	A59252	S21801	JC5837	T38077	A27605	A57107	T38435	833821	S30431	S43074
	DB	5	7	7	7	~	~	~	7	7	~	~	~	~	~	~	7	~	N	~	~	-	~	~	-	-	7	N	~	~
	Length	770	770	739	748	851	786	793	794	794	848	978	837	2094	533	1166	1208	1164	289	1690	1976	1999	3187	1957	3685	747	750	857	1178	968
df	Query	98.6	98.2	44.9	43.6	27.4	22.9	22.9	22.4	20.5	10.6	10.3	10.2	10.2	10.2	10.1	10.1	6.6	9.8	•	٠.	•	9.6	9.6	•	٠	9.5	9.5	٠	9.4
	Score	1156	1151	526.5	511	321	268.5	268.5	262.5	237	124.5	121	119.5	119.5	119	118.5	118.5	116	115	113.5	113	113	113	112.5	112	111.5	111.5	111.5	111.5	110.5
	Result No.		8	m	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT 2 A54444 DNA-binding protein APRF - human

myosin heavy chain	myosin heavy chain	myosin heavy chain	myosin heavy chain	hypothetical prote	myosin heavy chain	microtubule bindin	hypothetical prote	probable myosin he	SCP1 protein - rat	hypothetical prote	myosin heavy chain	myosin heavy chain	myosin heavy chain	nuclear/mitotic ap	M protein precure
806117	A33977	A47297	B43402	AC1814	A41604	H90279	T27055	F84730	\$28061	AE2304	A27224	A59287	MWKW	T30336	460115
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	9.4 1959	_	•		_			_		_		_	_	.,	
9.4	-	9.3	9.3	9.3	9.3	9.5	9.5	9.2	9.5	9.2	9.2	9.2	9.5	9.2	- 0

ALIGNMENTS

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Cipecies: Mus musculas (house)
Cipecies: Mus musculas (house)
Cipate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
R;Akira, S: Nishto, Y: Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su
Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a.novel IFN-stimulated gene factor 3 p91-related tr
A;Reference number: A54444; MUID:9420862; PMID:7512451
A;Accession: 149508
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;References: UNIPROT:P42227; GB:L29278; NID:G476715; PIDN:AAA37254.1; PID:G47671
A;Reference number: 149009; MUID:95014185; PMID:7523373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: I49009
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Ablocule type: mRNA
A;Residues: 1-393,'M',395-700,702-770 <RE2>
A;Residues: EMBL:U08378; NID:G473889; PIDN:AAA56668.1; PID:G473890
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
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98.6%; Score 1156; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 1.8e-69;
Matches 226; Conservative 1; Mismatches 2; Indels
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p91-related transcription factor - mouse
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A;Cross-references: EMBL:U18671; NID:g1293919; PIDN:AAA98760.1; PID:g1293920
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.B.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in
  250 GPPNACLDQLQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-851 < YAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-748 <YAM>
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C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46159
R;Schindler, C.; Fu, X.Y.; Improta, T.; Aebersold, R.; Darnell Jr., J.B.
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kba ISG
A;Accession: A46159; MUID:92366557; PMID:1502203
                                         C;Accession: A54444

C;Accession: A54444

S; Nishilo, Y:; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sud
Cell 77, 63-71, 1994

A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tra
A;Reference number: A54444; MUID:94208062; PMID:7512451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
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s: Homo sapiens (man)
21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                  A;Gene: GDB:STAT3; APRF
A;Cross-references: GDB:358950
A;Map position: 17q21-17q21
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator STATSA
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                                                                                                                                                           A;Accession: A54444
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Rolecule type: RES>
A;Cross-references: UNIPROT:P40763; GB:L29277; NID:G475788; PID:G475789
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1151; DB 2
Pred. No. 4e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: UNIPROT: P42224
                                                                                                                                                                                                                                                                                                                                                                                                                                               98.2%;
98.3%;
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Best Local Similarity 46.2%
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.3
Matches 225; Conservative
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                                                                                                                                                                                                                                                                               C;Genetics:
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C;Accession: A56047
R;Yamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, Mol. Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in e. A;Reference number: A56047; MUID:94277038; PMID:8007943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P42228; GB:U09351; NID:9509502; PIDN:AAA19692.1; PID:950950
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interferon alpha-induced transcription activator ISGF-3, 113K chain - human NyAlternate names: stat2 protein C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C;Accession: A46160; S71908; S53873 R;Fu, X.Y.; Schindler, C.; Improta, T.; Aebersold, R.; Darnell Jr., J.E. Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992 A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator A;Reference number: A46160; MUID:92366558; PMID:1502204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----QVRQQLKKLEELEQKYTYEHDPITKNKQVLWDRTFSLF 298
                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 VTRQXMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEIACIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 VTEKOOMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKS--QGDMQDLNGNNQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 748;
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                                                                           185 RNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                              gamma-interferon activation site-binding protein Stat4 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66; Indels
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                                                                                                                             299 QQLIQSSFVVERQPCMPTHPQRPLVLKTGVQFTVKLRLLVKLQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary, nucleic acid sequence not shown A;Wolecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 43.6%; Score 511; DB 2; Best Local Similarity 45.5%; Pred. No. 1.4e-26; Matches 102; Conservative 48; Mismatches 66;
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A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:248538; NID:g758633; PIDN:CAA8 R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L. Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved A;Reference number: 149273; MUID:96004632; PMID:7568026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S54772; I49273

K;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995

A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin-3, R;Reference number: S54772; MUID:95237198; PMID:7720707

A;Recession: S54772

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-793 <MUI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 RMSRETALOOKOVSLETWLOREAOTLOOYRVELAEKHOKTLOLLRKOOTIILDDELIOWK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 -----QSVTRQKMQQLEQML----TALDQMRRSIVSELAGLLSAMEYVQKTLTDEELA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 DWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 QWKRRQQLAGNGGPPEGSLDVLQSWCEKLAEIIWQNRQQIRRAEHLCQQLPIPG-PVEEM 312
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C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NATIcernate names: stat5 protein
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                        194 PQERMSRETALOQKQVSLETWLQREAQTLQQYRVELAEKHQKTLQLLRKQQTIILDDELI
                                                        AAVVTEKOOMLEQHAODVRKRVODLEOKMKVVENLODDFDFNY-KTLKSOGDMODLNGNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 LEERIVELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLV 224
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A;Residues: 1-793 <RES>
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A Residues: 1-786 <RES>
A Residues: 1-786 <RES>
A R. Cross-references: UNIPROT: P42232; UNIPROT: 09JKM1; EMBL: U21110; NID: 9747973; PIDN: AACSS R; Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A. BENDO J. 14, 1166-1175, 1995
EMBO J. 14, 1166-1175
EMBO J. 14, 1166-
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A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-432, 'E', 434-786 <MUI>
A;Cross-references: EMBI:Z48539; NID:g758635; PIDN:CAA88420.1; PID:g758636
R;Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris,
EMBO J. 14, 1402-1411, 1995
A;Title: Interleukin-3 signals through multiple isoforms of Stat5.
A;Reference number: S54725; MUID:95246733; PMID:7537213
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(Species: Mus musculus (house mouse)
Cjate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
CjAccession: 149274; SS4773; SS4773; S54727
R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Rytitle: Cloning and expression of Stats and an additional homologue (Stat5b) involved
A;Reference number: 149273; MUID:96004632; PMID:7568026
A,Reference number: S53873; MUID:95192056; PMID:7885841
A,Accession: S53873
A;Status: nucleic acid sequence not shown
A;Nolecule type: DNA
A;Residues: 1-156;392-591;684-730 <YAM>
A;Residues: 1-156;392-591;684-730 <YAM>
A;Residues: 1-156;392-591;684-730 <YAM>
A;Genetics:
A;Genetics:
A;Genetics:
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C;Genetics: A;Gene: stat2
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 RQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEIACIGGPP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 NICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 VTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.4%; Score 321; DB 2; Length 851; Best Local Similarity 33.5%; Pred. No. 7e-14; Matches 74; Conservative 51; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 LHRAFVVETQPCMPQTPHRPLILKTGSKFTVRTRLLVRLQE 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 MKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.9%; Score 268.5; DB 2; Best Local Similarity 30.6%; Pred. No. 2e-10; Matches 71; Conservative 42; Mismatches 98;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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conserved hypothetical protein aq_1006 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: OB-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: A70387
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Recence number: A70387

A;Accession: A70387

A;Stauus: preliminary: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-978 cAQP?

A;Kesidues: 1-978 cAQP?

A;Cross-references: UNIPROT:067124; GB:AE000718; NID:g2983504; PIDN:AAC07092.1; PID:g298/A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 IVSELAGLLSAMEYVOKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQ 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::::: | | | : : | | | : : | | | | 282 RIEEIDKKLTELKVRKNKLTKELAVLKOELSFAQEELNRIEABKEKFKEEKEREKELEHR 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLOETTGELEA----AKALVLKRIQIWKRQQQLAGNGAP-----FEESLAPLQER 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 TRQQIKKLEELQQKVSYKGDPI-VQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----DEELAD- 113
                                                                                                                                                                                                                                                                                                                                                         C, Accession: A54740
R, Hou, J.; Schindler, U.; Henzel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 EKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQ 69
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C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032
                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:P42226
C,Superfamily: human signal transducer and transcription activator STAT5A
C,Keywords: DNA binding; transcription regulation
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                                                                      316 VNATITDDISALVTSTFIIEKQP------PQVLKTQTKFAATVRLLV 356
                                 224
                                                                                                                                                                                                                                                                                                                                                                                                               Science 265, 1701-1706, 1994
A;Title: An interleukin-4-induced transcription factor: IL-4 stat. A;Reference number: A54740; MUID:94367369; PMID:8085155
A;Accession: A54740; MUID:94367369; PMID:8085155
A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
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                                 176 LEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52; Indels
                                                                                                                                                                                                                                                           interleukin-4-induced transcription factor stat - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 KMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 PLVIKTGVOFTTKVRLLV 224
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Best Local Similarity
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Matches
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                                        Kilin, J.

Submitted to the EMBL Data Library, December 1995

A;Reference number: H01043

A;Accession: G02317

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Molecule type: mLNA

A;Residues: 1-794 <LLN>

A;Cross-references: UNIPROT: P42229; EMBL: U43185; NID: g1151169; PIDN: AAB06589.1; PID: g115

C;Superfamily: human signal transducer and transcription activator STATSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55527; S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
BEMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regula
A;Reference number: S55527; MUID:95188889; PMID:7882987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-794 <WAK.
A; Cross-references: UNIPROT: P42231; EMBL: X78428; NID: g602354; PIDN: CAA55191.1; PID: g6023
A; Note: this is a revision to the sequence from reference S44353
R; Wakao, H.; Gouilleux, F.; Groner, B.
BMBO J. 13, 2182-2191, 1994
A; Title: Mammary gland factor (WGF) is a novel member of the cytokine regulated transcri
A; Reference number: S44353; MUID: 94244619; PMID: 7514531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || ::| |||| |::
257 RRQQLAGNGGPPEGSLDVLQSWCEKLAEIIWQNRQQIRRAEHLCQQLDIPG-PVEEMLAE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----OSVTROKMOQLEOML----TALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 RLSRETALQÓKOVSLEAWLOREAQTLOÓYRVELAEKHOKTLOLLRKOÓTIILDDELIOWK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 RRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 RLSRETALQÓKQVSLÉAWLQREAQTLQÓYŘVELAEKHQKTLQLLRKQÓTIILDDELIQWK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 RRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPM 175
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: this sequence has been revised in reference S5557
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 VTEKOOMLEOHAODVRKRVODLEOKMKVVENLODDFDFNY-KTLKSOGDMODL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 VNATITDIISALVTSTFIIEKQP------PQVLKTQTKPAATVRLLV 356
                                                                                                                                                                                                                                                                                                                                                  Query Match 22.4%; Score 262.5; DB 2; Length 794; Best Local Similarity 30.1%; Pred. No. 5.1e-10; Matches 69; Conservative 43; Mismatches 96; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.2%; Score 237; DB 2; Length 794; 29.3%; Pred. No. 2.5e-08; ive 42; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 LEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Residues: 1-716,'RHLHGPGSLPSR',729,'P',731,'ASL' <WAW>A,Cross-references: EMBL:X78428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: mRNA
C;Accession: G02317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: S44353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
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C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72593
C;Accession: G72593
C;Accession: G72593
C;Aill, 1999
C;Aill, 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q9YCP2; DDBJ:AP000061; NID:g5104821; PIDN:BAA80205.1; PID:d
A;Experimental source: strain Kl
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1447 ELKAQQDKVMETSAQSSGDHQE----QHVSVQEMQELKETLNQAETKSKSLESQ---- 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1497 --VENLOKTLSEKETEARNLOEQTVOLQSE----LSRLRODLODRTTOEEOLROOITEKE 1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 SAMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 TLKSQ------GDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLL 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --RVQDLEQKMKV---VENLQDDFDFNYK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X94208; NID:g1296797; PIDN:CAA63904.1; PID:g1296798 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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A; Molecule type: mRNA <MI2>
A; Residues: 1-725, L'. <MI2>
A; Cross-references: ENBL: X63105; NID: 937257; PIDN: CAA44819.1; PID: 937258
R; King, H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J.
A) Crossens 2, 617-619, 1988
A; Title: Tpr homologues activate met and raf.
A; Reference number: 800928; MUID: 88262257; PMID: 3387099
                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-31, "K', 33-142 < KIN>
A; Cross-references: EMBL: Y00672; NID: g37255; PIDN: CAA68681.1; PID: g37256
R; Greco, A.
Submitted to the EMBL Data Library, December 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
10.2%; Score 119.5; DB 2; Length 2
Best Local Similarity 20.4%; Pred. No. 5.1;
Matches 45; Conservative 50; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :| :::| :::|
1551 EKTRKAIVAAKSKIAHLAGVKDQLTKENEELKQRNGALDQQ 1591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 ELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein APE1216 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 VTEKQQMLEQHAQDVRKRVQDLEQKMKVVEN----LQDDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.2%; Score 119; DB 2; 20.7%; Pred. No. 1.1; iive 49; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:128821; OMIM:189940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: G01185
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 144-228 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 AVVTEKQQMLEQHAQDVRK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: H00592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 1q25-1q25
A;Introns: 177/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 41; Conserva
                                                                                                                                                                                                                                                                              A;Accession: S00928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB: TPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: APE1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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C; Date: 22-Nov-1993 #sequence revision 26-May-1995 #text_change 09-Jul-2004
C; Date: 22-Nov-1993 #sequence revision 26-May-1995 #text_change 09-Jul-2004
C; Accession: S3124; S22740; S
Oncogene 7, 2329-2333, 1992
A; Title: The human typ: gene encodes a protein of 2094 amino acids that has extensive coin A; Reference number: S33124; MUID:93064711; PMID:1437155
A; Accession: S3124
A; Reference number: S33124; MUID:93064711; PMID:1437155
A; Accession: S3324
A; Residues: 1-2094 cMIT>
A; Residues: 1-2094 cMIT>
A; Residues: 1-2094 cMIT>
A; Cooper, C.S.
Oncogene 7, 383-388, 1992
A; Title: Nucleotide sequence was submitted to the EMBL Data Library, October 1991
B; Mitchell, P.J.; Cooper, C.S.
Oncogene 7, 383-388, 1992
A; Title: Nucleotide sequence analysis of human tpr CDNA clones.
A; Reference number: S23740; MUID:92195670; PMID:1549355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CiAccession: 157557
Riguelle, Fw.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M.; Cleve Riguelle, Fw.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M.; Cleve Mol. Cell. Biol. 15, 3336-3343, 1995
A;Title: Cloning of murine Stat6 and human Stat6, Stat proteins that are tyrosine phosph A;Reference number: 157557; MUID:95280934; PMID:7760829
A;Accession: 157557; MUID:95280934; PMID:7760829
A;Accession: 157557
A;Molecule type: mRNA
A;Residues: prellminary; translated from GB/EWBL/DDBJ
A;Cross-references: UNIPROT:P52633; GB:L47650; NID:gl008876; PIDN:AAA79006.1; PID:gl0088
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tpr protein - human
N;Alternate names: kinase-related transforming protein (tpr-met); protein with promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                       WKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHR 173
                                                                               253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 D-----LNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMBYVQKTLTDEELA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 NLIDPPLNGPGPS------EDLPTILQ-------GTVGDLETTQ-PLVLLRIQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 DWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLE-ELQQKVSYKGDPIVQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Mus musculus (house mouse)
Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
Accession: I57557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 EKQOMLEQ--HAQDVRKRVQD-----LEQKMKVVENLQDDFDFNYKTLKSQGDMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 IWKRQQQLAGNGTPFEESLAGLQERCESLVEIYSQLHQEIGAASGELEPKT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 HRPMLEERIVELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-Binding Protein and transcription factor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.2%; Score 119.5; Dilarity 25.8%; Pred. No. 1.7; Conservative 31; Mismatches
                                                                                                                                                                                          174 PMLEERIVELFRN-----LMKSAFVVERQ 197
                                                                                                                                                                                                                                                                  394 EEKLEKIKELFSEEEYTSLKMKERLLVELQ 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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A;Gene: CESP:Y51A2D.16
A;Map position: 5
A;Introns: 17/3; 45/1; 76/2; 156/3; 240/2; 288/2; 594/2; 657/3; 756/3; 798/2; 900/3; 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rimcharay, A.

Submitted to the EMBL Data Library, January 1998

A; Reference number: 220307

A; Accession: T27075

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Residues: 1-1166 <WIL>
A; Cross-references: EMBL:AL021497; PIDN:CAA16403.1; GSPDB:GN00023; CESP:YS1A2D.16

A; Experimental source: clone Y51A2D
                                 ::| ::||| ::||| 379 LAEAQASLEDLNTRLDQVA-STLQQLQQRLATAEESLQALTEDLASLQAEVETLQQSIVE 437
                                                                                                                                         : | :: | :: | :: | 490 NDLKTCQTQLELES------KKLQRLREDLVLEKSRRADLIGRIHSLCTTLSLNGA 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         540 NFEKINNDDELIDNIDDIMMALVAVKRERDDIRIQGNQQIQELHDLKRDIEKLRRSESE 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            600 SLNESDDRVRELTRENMHTKEQVFMLQEKLRELNLELSTKNDEI----DMVKASIEELNR 655
49 TLKSOGDMODLNGNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTD 108
                                                                                                     109 EELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQ----TRQQIKKLEELQQKVSY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 FNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEY--- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 -VQKTLTDEELAD--------WKRRPEIACIGGPPNI----------129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 CLDRLENWITSLAESQLQTRQQI----KKLEELQQKVSYKGDPIVQHRPMLEERIVELFR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NHPTAAVVTEKQ----QMLEQHAQ------DVRKRVQDLEQKMKVVENLQDDFD 44
                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Y51A2D.16 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75; Indels 69; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
10.1%; Score 118.5; D
Best Local Similarity 20.7%; Pred. No. 3;
Matches 50; Conservative 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: May 25, 2005, 17:45:29 Job time : 22.6038 secs
                                                                                                                                                                                                              165 KGDPIVQHRPMLEERIVE 182
                                                                                                                                                                                                                                         : | |:|: |
-----ELRTQLDEKTRE 497
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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 25, 2005, 17:15:30 ; Search time 95.284 Seconds

(without alignments)

1230.701 Million cell updates/sec
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Title:

Perfect score: 1172
Sequence: 1 NHPTAAVVTEKQQMLEQHAQ.....IKTGVQFTTKVRLLVKFPEL 229
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Listing first 45 summar.
Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		P42227 mus musculu	P52631 rattus norv		Q6dv79 gallus gall		Q7zxk3 xenopus lae	Q7zts5 brachydanio		Q6gue7 oryzias lat			Q90y16 tetraodon f	O13133 oncorhynchu	Q9n145 macaca mula	Q8jgn0 xenòpus lae	Q6p6g7 rattus norv	Q9qxk0 rattus norv	Q8c497 mus musculu	Q99k94 mus musculu	Q8c3v4 mus musculu	Q9d323 mus musculu	Q8c8m3 mus.musculu	P42224 homo sapien	Q68d00 homo sapien	Q764m5 sus scrofa	P42225 mus musculu	O13131 oncorhynchu	093598 brachydanio	Q6p943 brachydanio	Q8jfu8 brachydanio
SUMMARIES	ID	STA3 HUMAN	STA3 MOUSE	STA3_RAT	STA3_BOVIN	Q6DV <u>7</u> 9	Q9PVX8	Q7ZXK3	Q7ZTS5	Q6DVF3	Q6GUE7	Q6NV46	093599	Q90Y16	013133	Q9N145	Q8JGN0	Q6P6Q7	Q9QXK0	Q8C497	Q99K94	Q8C3V4	090323	Овсвиз	STA1 HUMAN	Q68D <u>0</u> 0	Q764M5	STA1 MOUSE	013131	093598	Q6P943	QBJFUB
	DB	-	Н	-	Н	~	~	~	7	~	~	7	~	7	~	7	~	~	7	~	7	7	~	7	Н	8	~	-	~	7	~	7
	Query Match Length DB	770	770	770	770	771	769	166	414	765	785	786	806	764	767	163	751	712	749	749	712	749	749	755	750	750	757	749	754	749	749	528
de	Query Match	98.6	98.6	98.4	98.0	96.5	93.7	93.4	86.2	86.2	86.2	86.2	86.2	84.1	83.3	56.0	49.3	49.1	49.1	49.0	48.9	48.9	•	•	48.8	48.8		•	46.2	45.6	45.6	45.6
	Score	1156	1156	1153	1149	1131	1098	1095	1010	1010	1010	1010	1010	986	916	929	578	576	576	574	573	573	573	573	572	572	572	565	541.5	535	535	534
	Result No.	7	7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

_			Q90y17 tetraodon f		Q8aw24 brachydanio	P42228 mus musculu	Q7zz53 brachydanio	Q8aw20 brachydanio	Q7zz77 brachydanio	Q8jfu7 brachydanio	Q66hb2 rattus norv	Q8jf85 brachydanio	Q90y15 tetraodon f
Q704W6	Q801Y2	STA4 HUMAN	Q90Y17	013132	Q8AW24	STA4 MOUSE	Q7ZZ <u>5</u> 3	QBAW20	072277	Q8JFU7	066нв2	QBJFSS	Q90Y15
~	~	Н	N	~	7	-	~	7	7	7	7	0	~
108	718	748	758	754	657	749	651	667	652	553	748	1153	737
45.4	45.3	44.6	44.4	44.2	44.0	43.3	43.3	43.3	43.2	43.2	43.2	43.0	42.2
2.5	530.5	523	520.5	518.5	516	507.5	507	507	506.5	206	206	504	494
53													

ALIGNMENTS

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### STATE | PRT | 770 AA.

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**AC PROTEST | OFFICE | OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 102582; -.
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0005632; F:hematopoietin/interferon-class (D200-domain. . .; TAS.
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez, A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I. Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                       PubMed=11773079; DOI=10.1074/jbc.M111486200;
PubMed=11773079; DOI=10.1074/jbc.M111486200;
Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
"Functional interaction of STRAT3 transcription factor with the coactivator NCoA/SRC1a.";
J. Biol. Chem. 277:8004-8011(2002).
-I. FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6) responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                acute-phase protein genes.
--- PATHMAY: Involved in the gpl30-mediated signaling pathway.
--- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOAI.
--- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
                                                                                                                                                                                                                   PHOSPHORYLATION ON SERINE.
MEDIATE=5921644; PubMed=7701321;
ARADIATE=5921644; PubMed=7701321;
ARADIATE=5921644; PubMed=7701321;
ARADIATE=901644;
ARADIATE OF SERINE PHOSPHORYLATION for formation of STAT-promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Del-701;
ISOId=P40763-2; Sequence=VSP_010474;
-:- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  muscle, kidney and pancreas.

This Tycosine phosphorylated in response to IL-6, IL-11, CNTF, ILF, CSF-1, EGF, DGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 is important for the framscribtional activity.

SIMILARITY: Belongs to the transcription factor STAT family. SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                      ö
                                                                                                                                                                     Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P40763-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in response to phosphorylation. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ012463; CAA10032.1; -. AY572796; AAS66986.1; -. BC000627; AAH00627.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC014482; AAH14482.1; -. AF029311; AAB84254.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L29277; AAA58374.1; -.
                                                                                                                                          SEQUENCE OF 564-704 FROM N.A.
                                                                                                                                                                                                                                                                                            Science 267:1990-1994(1995).
                                                                                            and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC:11364; STAT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A54444; A54444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFAC; T01493; -.
                                                                                                                                                           TISSUE=Liver;
                                                                                                                                                                                                                                                                                   complexes."
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NHPTAAVVTEKQOMIEOHLODVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNNOSVTROKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 ACIGGPPNICLDRLENWITSLABSQLQTRQQIKKLEBLQQKVSYKGDPIVQHRPWLEERI 309
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GO; GO:0003700; F:transcription factor activity; TAS.

GO; GO:000528; P:cell motility; TAS.

RO; GO:000725; P:DAX Cascade; TAS.

GO; GO:000125; P:DAX Cascade; TAS.

GO; GO:0007129; P:negrative regulation of transcription from P. .; TAS.

RO; GO:0007165; P:signal transduction; TAS.

TherPro; IPR0009807; PSJ like_DNA_bnd.

R InterPro; IPR00019807; PSTAT.

R Fam; PF0017; STAT.

R Fam; PF0017; STAT alpha; 1.

R Fam; PF02864; STAT_bind; 1.

R PF0S864; STAT_bind; 1.

R PKOSITE; PSS0001; SH2; 1.

R Activator; Alternative splicing; DNA-binding; Nuclear protein;

R Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
                                                                     .; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
                                                                                                                                                                                                                                                                                                                                                                          Phosphotyrosine (by JAK) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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STRAIN-BALB/c; TISSUE-Liver;
MEDLINE-94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
signal transducer and activator of transcription 3 (Acute-phase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.6%; Score 1156; DB 1; Length 770; 98.7%; Pred. No. 3.1e-65; ive 1; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                Phosphoserine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (in isoform Del-701)
/FIId=VSP_010474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F -> Y (in Ref. 1).
V -> L (in Ref. 1).
T -> A (in Ref. 1).
; 6C00632211C8012D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            O -> K (in dbSNP:1803125)
/FTId=VAR_018683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q -> H (in Ref. 1).
P -> S (in Ref. 1).
K -> N (in Ref. 1).
F -> Y (in Ref. 1).
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/FTId=VAR
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Name=Stat3; Synonyms=Aprf;
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Matches 226; Conservative
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ID STA3_MOUSE
AC P42227;
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us-10-090-185-30.rup

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CSTRAIN=EVBN/N; TISSUE=Mammary gland;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MAIschul S.F., Zeeberg B., Baccow K.H., Schaefer C.F., Bhat N.K.,

MAIschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

MAIschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

MAISCHON M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Myilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Mutterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Mand Munic Chan and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                       MEDLINE=95014,185; PubMed=7523373;
Raz R., Durbin J.E., Levy D.E.;
"Acute phase response factor and additional members of the interferon-stimulated gene factor 3 family integrate diverse signals from cytokines, interferons, and growth factorse.";
J. Biol. Chem. 269:24391-24395(1994).
                                                                                                                                                 Zhong Z., Wen Z., Darnell J.E. Jr., "Staff; a STAT family member activated by tyrosine phosphorylation in response to epidermal growth factor and interleukin-6."; Science 264:95-98(1994).
Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T., Yoshida K., Sudo T., Naruto M., Kishimoto T.; "Molecular cloning of ARRF, a novel IFN-stimulated gene factor 3 p91-related transcription factor involved in the gpl30-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM STAT3B).
STRAIN=BALB/c, and CS7BL/6; TISSUE=Liver;
MEDLINE=96016116; PubMed=7568080;
SChaefer T.S., Sanders L.K., Nathans D.;
"Cooperative transcriptional activity of Jun and Stat3 beta, a short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11161808; DOI=10.1006/geno.2000.6433;
Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T.,
Dewar K., Henighausen L.;
"Structure of the mouse stat 3/5 locus: evolution from Drosophila to
zebrafish to mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6J, and NOD/LtJ;
Davoodi-Semiromi A., She J.-X.;
A mutant StatSb with weaker DNA binding defines a key defective pathway in non-obese diabetic (NOD) mice.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS
                                                                                                       SEQUENCE FROM N.A. (ISOFORM STAT3A).
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                                                                                                                                     MEDLINE=94188718; PubMed=8140422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics 71:150-155(2001).
                                                                         Cell 77:63-71(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Stat3."
                                                                                                                                                                                                                                             TISSUE=Brain;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IL-6)-responsive elements identified in the promoters of various acute-phase protein genes. STAT3B interacts with the N-terminal part of JUN to activate such promoters in a cooperative way.

-!- PATHWAY: Involved in the gpl30-mediated signaling pathway.
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.
MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9; Wen Z., Zhong Z., Darnell J.E. Jr.; Wen Z., Zhong Z., Darnell J.E. Jr.; "Maximal activation of transcription by Statl and Stat3 requires both tyrosine and serine phosphorylation."; Cell 82:241-250(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P4227-3; Sequence=VSP 010475;
IsoId=P4227-3; Sequence=VSP 010475;
TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and kidney. STAT3B is also detected in the liver, although in a much less abundant manner.

FYM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, IF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity (By similarity). SIMILARITY: Belongs to the transcription factor STAT family. SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                  "Three-dimensional structure of the Stat3beta homodimer bound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pro.
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GO; GO:0005737; C:cytoplasm; IDA.

GO; GO:0005634; C:nucleus; IDA.

GO; GO:0005634; C:plasma membrane; IDA.

GO; GO:0005815; P:DNA binding; IDA.

GO; GO:0005515; P:protein binding; IPI.

GO; GO:0005515; P:transcriptional activator activity; IDA.

GO; GO:0007559; P:JAK-STAT cascade; IDA.

GO; GO:0007557; P:requlation of transcription from Pol II E
                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;
Becker S., Groner B., Mueller C.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Stat3B;
IsoId=P42227-2; Sequence=VSP_006287;
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InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF01017; STAT alpha; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EWBL; L29278; AAA37254.1; -
EWBL; U06922; AAA19452.1; -
EWBL; U069378; AAA16468.1; -
EWBL; U30709; AAC55612.1; -
EWBL; AF246978; AAL59017.1; -
EWBL; AY29489; AAC75418.1; -
EWBL; AY29480; AAC75418.1; -
EWBL; AY29480; AAC75419.1; -
EWBL; BC003806; AAH03806.1; -
PIR; 149508; 149508.
PIR; 149508; 149508.
TRANSFRC; T01574; --
MGD; MGI:103038; Stat3.
                                                                                                                                                                                                                                                                                                                                                                                                            DNA.";
Nature 394:145-151(1998)
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Transcription regulation.
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                                Fey G.H.;
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                                                                                                                                                                                                                                                                                                                                                         130 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN 189
                                                       Phosphoserine.
TTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
                                                Phosphotyrosine (by JAK) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                    61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                          ACIGGPPNICLDRLENWITSLARSQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Stat3;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                           1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                       FDMDLTSECATSPM -> FIDAVWK (in isoform
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                                                                                     /FTIC=VSP 006287.
Missing (In isoform Del-701).
/FTId=VSP_010475.
S->A: Decreased transcriptional
                                                                                                                                                                                                                                                                                                           Length 770;
Pfam; PF02865; STAT_int; 1.
PROSITE; PS50001; SH2; 1.
3D-etructure; Activator; Acute phase; Alternative splicing; Direct protein sequencing; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain; Transcription regulation.
DOMAIN SH0.
                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                             E -> K (in Ref. 2).
S -> T (in Ref. 2 and 4).
M -> I (in Ref. 1).
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01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                                                           98.6%; Score 1156; DB 1;
ilarity 98.7%; Pred. No. 3.1e-65;
Conservative 1; Mismatches 2;
                                                                                                                       activation.
                                                                                Stat3B)
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Matches 226; Conserv
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P52631;
                                                MOD_RES
MOD_RES
VARSPLIC
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                                                                                             "Transcription factors Stat3 and Stat5b are present in rat liver nuclei late in an acute phase response and bind interleukin-6 response
                                                                                                                                                                                                                                                                                Pfam; PP00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02865; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                               elements.";
J. Biol. Chem. 270:29998-30006(1995).
-!- FUNCTION: Transcription factor that binds to the interleukin-6
(IL-6)-responsive elements identified in the promoters of various
MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998; Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            705 705 Phosphotyrosine (by JAK) (By 727 727 Phosphoserine (By similarity) 770 AA; 88039 MW; D74AOC76954754ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X91810; CAA62920.1; -.
HSSP; P4227; 1BG1.
RGD; 3772; Stat3.
InterPro; IPR008967; P53_like_DNA_bnd.
InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GNNOSVTROKMOQLEOMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Transcription factor that binds to the interleukin-6
(IL-6) -responsive elements identified in the promoters of various acute-phase protein genes (By similarity).
-!- PATHWAY: Involved in the gpl30-mediated signaling pathway.
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOA1 (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation (By similarity).
-!- SIMILARITY: Belongs to the transcription factor STAT family.
-!- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 GNNQSVIRQKWQQLEQMLIALDQMRRSIVSELAGLLSAMEYVQKTLIDEELADWKRRQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSS0001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphotyrosine (by JAK) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Mammary gland;
Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
"The STAT5B-encoding gene was flipped across the STAT3/STAT5A-locus during ruminant evolution.";
                                                                                                                                                                                                                              Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VELFRNLAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.0%; Score 1149; DB 1; Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphoserine (By Similarity)
9CEB147C73E83274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                  05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
55-OCT-2004 (Rel. 45, Last annocation update)
55-GDA (Rel. 45) Last annocation update)
Signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 8.6e-65;
1; Mismatches 3
                      770 AA.
                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ620655; CAF06182.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      770 AA; 87974 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 98.3%;
nes 225; Conservative
                      STANDARD;
                                                                                                                                                                                                           Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                      Bovinae; Bos
                      BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
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Q6DV79
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771 AA

PRT;

PRELIMINARY;

Q6DV79 Q6DV79;

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251 CIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLBERIV 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 CIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIV 181
                                                                                                                                                                                                                                                  14. SEQUENCE FROM N.A.

15. SEQUENCE FROM N.A.

16. Zhou G.Y., Leung F.C.;

17. Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

18. GO; GO:0005634; C:nucleus; IEA.

19. GO; GO:0007242; P:intracellular signaling cascade; IEA.

19. GO; GO:0007242; P:intracellular signaling cascade; IEA.

19. GO; GO:0007242; P:intracellular signaling cascade; IEA.

19. Rob; GO:0007242; P:intracellular signaling cascade; IEA.

19. InterPro; IPR00980; SH2.

19. RinerPro; IPR001217; STAT.

19. Pfam; PF001017; STAT alpha; 1.

19. Pfam; PF01017; STAT alpha; 1.

19. Pfam; PF02864; STAT lint; 1.

19. Pfam; PF02865; STAT lint; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNG
                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
Nishinakamura R., Mateumoto Y., Matsuda T., Ariizumi T., Heike T.,
Asashima M., Yokota T.;
"Activation of Stat3 by cytokine receptor gpl30 ventralizes Xenopus embryos independent of BMP-4.";
Dev. Biol. 216:481-490(1999).
EMBL; AB017701; BAA86061.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88174 MW; 71AC855C5DEC03E2 CRC64;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                 Signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1131; DB 2;
Pred. No. 1.2e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              769 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 221; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02865; STAT ir
PROSITE; PS50001; SHZ;
SEQUENCE 771 AA; 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACIGGPPNICLDRLENWITSLAESQLQTRQQIRKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                 00; 00:0005634; C:nucleus; IEA.

00; 00:0005634; C:nucleus; IEA.

00; 00:0003700; F:transcription factor activity; IEA.

00; 00:0003700; F:transcription factor activity; IEA.

00; 00:000355; P:tregulation of transcription, DNA-dependent; IEA.

00; 00:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000867; PS3 like_DNA_bnd.

InterPro; IPR00137; STAI.

InterPro; IPR00137; STAI.

Pfam; PF001017; STAI alpha; 1.

Pfam; PF001017; STAI alpha; 1.

Pfam; PF02865; STAI alpha; 1.

Pfam; PF02865; STAI int; 1.
                                                                                                 MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
                                                                                                                                                         'Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTNKVRLLVKFPEL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VELFRNIAMSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 93.4%; Score 1095; DB 2; Length 7 Best Local Similarity 91.7%; Pred. No. 2.3e-61; Matches 210; Conservative 11; Mismatches 8; Indels
                                                                                                                                                                                                                                              TISSUE=Embryo;
Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO44717; AAH44717.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87599 MW; 31018A3321CCEB9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                            Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                  mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00252; SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       766 AA;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyprinidae; Dani
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stat3 protein.
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                                                                                                                                                                             initiative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250
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PROSITE;
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Q7ZTS5;
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WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., MaxS.I., Wang J., Hsieh F.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Aspleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Browstein M.J., Uddin T.B., Toshiyviki S., Carninoi P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                         130 SHPNAAVVTEKQQMLEQHLQDVRKKVQDLEQKMKVVENLQDDFDFNYKTLKSQSDLSELN
                                                                                                                                                                                                                                                                                                                                                                                                                                              GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                         Gaps
            GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004871; F:signal transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000867; P53 like_DNA_bnd.
InterPro; IPR0017; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoldea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                Score 1098; DB 2; Length 769;
Pred. No. 1.5e-61;
9; Mismatches 8; Indels C
                                                                                                                                                                                                                                                ;50001; SH2; 1.
769 AA; 87974 MW; 0905C03263303069 CRC64;
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Last annotation update)
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                                                                                                                                                         Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
                                                                                                                                                                                                                                                                                                93.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7ZXK3;
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                         Pfam; PP02865; STAT_int; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 769 AA; 87974 M
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                  Best Local Simi
Matches 212;
                                                                                                                                                                                                                                                                                                    Query Match
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SEQUENCE
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            SON THE PROPERTY OF THE PROPER
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altasner R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D.,
Altechul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.K.,
Abtachench L., Marusiaa K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
And J. Helton B.K., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Nahiting M., Andan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Abriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Aones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 IACIGGPPNICLDRLETWITSLAESQLQIRQQIRKLEELQQKVSYKGDPIIQHRPALEEK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 HPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005634; C:nucleus; IEA.

GO; GO:0004871; F:signal transducer activity; IEA.

GO; GO:0004871; F:transcription factor activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR007157; STAT.

InterPro; IPR001217; STAT.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Signal transducer and activation of transcription factor 3.
Oryzias latipes (Wedake fish) (Japanese ricefish).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 IVELPRNIMKSAFVVEROPCMPMHDDRPLVIKTGVOFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC045276; AAH45276.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eam;
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QEDVF3
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61 GNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 HPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation 3 isoform 1.
05-JUL-2004 (TrEMBLrel. 27, Last annotation 3 isoform 1.
0ryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu R., Hong Y.;
Liu R., Hong Y.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AX641434; AAT46364.1; -
GO, GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0001700; F:transcription factor activity; IEA.
GO; GO:0007325; P:transcription factor activity; IEA.
GO; GO:000555; P:transcription of transcription, DNA-dependent; IEA.
InterPro; IPR0009867; FS3_like_DNA_bnd.
InterPro; IPR001217; STAT.
                                                                                                                                                                                     Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

BMBL; AR39947; AR164912.11 --

GO; CO:0005634; C:nucleus; IRA-

GO; GO:0004871; F:signal transducer activity; IEA-

GO; GO:0003700; F:transcription factor activity; IEA-

GO; GO:0007242; P:intracellular signaling cascade; IEA-

GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 IVDLFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTNKVRLLVKFPEL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha,
Beloniformes, Adrianichthyidae, Oryziinae, Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.2%; Score 1010; DB 2;
84.3%; Pred. No. 5.6e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR008967; P53_like_DNA_bnd.
InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
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Pfam; PF01017; STAT_alpha; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               765 AA;
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                                                                                                                             SEQUENCE FROM N.A.
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                                                              NCBI_TaxID=8090;
                                                                                                                                                              Hong Y.;
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86.2%; Score 1010; DB 2;
84.3%; Pred. No. 5.9e-56;
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Ffam; PP01017; STAT alpha; 1.
Ffam; PP02864; STAT bind; 1.
Pfam; PP02865; STAT_int; 1.
PROSITE; PS000252; SH2; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 806 AA; 92151 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=stat3;
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                                                                                                                                                                                                                                                                                                                                                                                      61
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093599
     88888888888888888
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XX MIGHINE-22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

XI TISSUE-Kidney,

XI Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Haieh F.,

Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Haieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

And Minish M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

And Mourse Chara M.A.,

"And Mourse Chara M
                                                                                                                                                                                     120 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                2 HPTAAVVTEKOOMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                    180 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                          DB 2; Length 785;
                                                                                        Query Match 86.2%; Score 1010; DB 2; Length 7 Best Local Similarity 84.3%; Pred. No. 5.7e-56; Matches 194; Conservative 20; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Kidney,
Straubberg R.;
Straubberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC064320; AAH68320.1; -.
ZFIN; ZDB-GENE-980526-68; stat3.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
                                             50001; SH2; 1.
785 AA; 89643 MW; 81F231BDE27DE938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 786 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
PROSITE; PSS0001; SH2; 1.
SEQUENCE 785 AA, 89643 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stat3 protein.
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05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=stat3;
                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 IACIGGPPNICLDRLETWITSLAESQLQIRQQIRKLEELQQKVSYKGDPIIQHRPALEEK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPTAAVVTEKOOMLEQHAODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDM-ODLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oates A.C.;
Thesis (1998), University of Melbourne, Australia.

EMBL; AJ005693; CAA06677.1;

R ZFIN; ZDB-GENES-980526-68; Stat1.

R ZFIN; ZDB-GENES-980526-68; Stat1.

R GO; GO:00005634; C:nucleus; EA.

GO; GO:0001742; F:signal transducer activity; IEA.

R GO; GO:0007242; P:intracellular signaling cascade; IEA.

R GO; GO:0007242; P:intracellular signaling cascade; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR000980; SH2.

R InterPro; IPR0001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00896; SH2.
InterPro; IPR00980; SH2.
InterPro; IPR001317; STAT.
Pfam; PF0017; SH2: 1.
Pfam; PF02864; STAT alpha; 1.
Pfam; PF02865; STAT bind; 1.
Pfam; PF02865; STAT bind; 1.
PROSITE; PSS0001; SH2: 1.
PROSITE; PSS0001; SH2: 1.
SEQUENCE 786 AA; 90039 MW; FC7371D0B0E5447E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 IVDLFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.2%; Score 1010; DB 2; Length 786; Best Local Similarity 84.3%; Pred. No. 5.7e-56; Matches 194; Conservative 21; Mismatches 13; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 806;
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; 92151 MW; 74BC4EA401C3C942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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SHPSGTVVTEKQQILEHNLQDIRKRVQDMEQKMKMLENLQDDFDFHYKTLKSQGELSQDM 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STACTIGGPPKICLDRLETWITSLGEIOLOIROOIKKLEELOOKVSYKGDPIIOHRPALEE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDL
                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007342; P:interacellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008967; PS3 like_DNA_bnd.
InterPro; IPR001717; STAT.
                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei; Euteleostei, Protacanthopterygii, Salmoniformes, Salmonidae, Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ol-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Signal transducer and activator of transcription (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele.
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                            Johnson M.C., Mourich D.V., Leong J.C.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U6033; AAB60926.1; --
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arredondo J.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;
                                                                                                                                                                  Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.3%; Score 976; DB 2.
81.0%; Pred. No. 8e-54;
iive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta (Rhesus macaque).
                                                                        01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 81.0
Matches 187; Conservative
                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                               FROM N.A.
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                                                                                                                                                 Name=rbtStat3;
                                                                        01-JUL-1997
01-JUL-1997
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                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                              120 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                     GNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPF 119
                                                                                                                                                                                                        250 IACIGGPPNICLDRLETWITSLAESQLQIRQQIRKLEELQQKVSYKGDPIIQHRPALEEK 309
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                                  2 HPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 HPTAAVVTEKOOMLEQHAODVRKRVODLEOKMKVVENLODDFDFNYXTLKSOGDM-ODLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQXTLTDEELADWKRRPE
 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005634; Crucleus; IEA.
GO; GO:0005634; Crucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes; Tetradontoidea, Tetradontiformes;
                                                                                                                                                                                                                                                      IVELFRNIAMKSAFVVERQPCAPAHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 764;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307106; AAL09415.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87411 MW; E661FFE18BEFD8BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.1%; Score 986; DB 2;
83.0%; Pred. No. 1.8e-54;
                                                                                                                                                                                                                                                                                                                                                                                          764 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Mismatches
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retraodon fluviatilis (Puffer fish)
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                764 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=47145;
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Search completed: May 25, 2005, 17:43:44 Job time : 96.284 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild type Val substituted with Ala corresponds 151 position of Stat-3 protein" 213. .23 tat-3 frotein" /note = "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription, cellular transformation; dysproliferative disease; cancer; psoriasis;
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AAY72848
AAY72852
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                                                                                                                                                                                                                                                                                                                                                                                                           AAY72863 standard; protein; 229
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 Misc-difference
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Human
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          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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AAE22055
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by replacing Val 151 with Ala in Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c.Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, bNA binding domain, linker domain, SH2 domain and transactivation domain
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/note= "Stat3-c-Jun interaction region 1; corresponds
/note= "Stat3-c-Jun of Stat3 protein"
213...229
                                                                                                                                                                                                                                                                        NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Stat3-c-Jun interaction region 2; corresponds 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                   1 NHPTAAVVTEKOOMLEQHLODARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                             GNNOSVTROKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
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                                                                                                                                                                                      Length 229;
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                                                                                                                                                                                     ; Score 1172; DB 4;
; Pred. No. 6.5e-100;
0; Mismatches 0;
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                                                                                                                                                                                        100.0%;
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Matches 229, Conservative
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                                                                                                                                                           Sequence 229 AA;
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/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"
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                                                                                                                                                                                                                                                                                                                                                    1 NHPTAAVVTEKQQMLEQHLQDVRKKVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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Pred. No. 1.5e-99;
0; Mismatches 1; Indels
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/note= "Stat3-c-Jun interaction region 2;
342-358 position of Stat3 protein"
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              65; Page 76-77; 86pp; English.
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Best Local Similarity 99.6%;
Matches 228; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                        Sequence 229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200116605-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY72846;
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             Claim
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31-AUG-1999;
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24-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR72082;
                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                       The present sequence is mouse Stat3 protein fragment containing 107-358 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of typroliferative diseases and also for treating cancer and psoriaeis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /notes "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein" 236. .252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ដ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                   24 NHPTAAVVIEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Stat3-c-Jun interaction region 2; corresponds 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                           84 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                               1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKWKVVENLQDDFDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                              61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                            121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                 Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                 Length 252;
                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse Stat3 protein fragment #2 (107-377 amino acids).
                                                                                                                                                                                                                                                               Score 1168; DB 4;
Pred. No. 1.7e-99;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                    Claim 65; Page 73; 86pp; English
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                                                                                                                                                                                                                                                               99.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2001 (first entry)
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.6
Matches 228; Conservative
                                                                                                                                                                                                                                        Sequence 252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200116605-A2
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61 GNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is mouse Stat3 protein fragment containing 107-377 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of transformation of sleases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                           Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.7%; Score 1168; DB 4; Length 271; 99.6%; Pred. No. 1.9e-99; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVQFTTKVRLLVKPPEL
                                                                                                                                         Darnell JE;
                                                                                                                                         Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                    Claim 65; Page 67-68; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR72082 standard; protein; 770 AA
99US-00387418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-US010849
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Matches 228; Conservative
                                                                    (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                         Zhang X, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse Stat3 (19sf6).
                                                                                                                                                                                                          WPI; 2001-226705/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-SEP-1994;
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27-SEP-1995
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121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPWLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .25
/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"
                                                                                                                                                                                                             New STAT protein DNA-binding domain peptide(s) - useful for diagnosing, preventing or treating cellular dysfunction, e.g. oncogenesis, inflammation, parasitic disease or autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                        Mouse signal transducer and activator of transcription (STAT) protein STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from ligand-activated receptor kinase complexes followed by nuclear translocation and DNA binding to activate transcription. Recombinant STAT4 can be obtd. using cDNA clone 19sf6 (AAT31278) obtd. from splenic/thymic cells. STAT4 includes a DNA-binding domain (see also haw03167) capable of both receptor recognition and message delivery vi DNA binding in a receptor-ligand specific manner. STAT proteins and the DNA binding domains (see also AAW03165-75) are useful for screening antagonists used to inhibit STAT-mediated signal transduction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NHPTAAVVTEKOOMLEQHLQDARKRVQDLEQKWKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNNQSVTRQKMQQLEQMLTALDQMRRSIVSBLAGILLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.7%; Score 1168; DB 2;
99.6%; Pred. No. 7.5e-99;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                           Disclosure; Page 87-90; 138pp; English.
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                                                                                                                          Horvath CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY72862 standard; protein; 229
               95WO-US017025
                                                    95US-00369796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activation of transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy; mutant; mutein.
                                                                                   (UYRQ ) UNIV ROCKEFELLER
                                                                                                                            Wen Z,
                                                                                                                                                               WPI; 1996-333941/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                  N-PSDB; AAT31280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                          Darnell JE,
               28-DEC-1995;
                                                    06-JAN-1995;
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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                                                                                                                                                                                                                                                                                       A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in AAQ89338) was isolated that encoded a 91 KDa protein (AAR72080) (Stat1) that was responsive to interferon-gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AAQ89339 +40) were cloned in plasmids 138fl and 198f6 and encoded proteins termed Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                  Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.7%; Score 1168; DB 2; Length 770; 99.6%; Pred. No. 7.5e-99; ive 0; Mismatches 1; Indels (
                                                                                             Ζ;
                                                                                             Zhong
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/label= DNA binding_domain
/note= "Claim 3, page 110"
                                                                                               Wen
                                                                                                                                                                                                                                                              Claim 1; Page 107-110; 160pp; English.
                                                                                               X,
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                                                                                               Shuai
   94US-00212184.
94US-00212185.
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                                                                                               Schindler CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 99.6
Matches 228; Conservative
                                                        UYRQ ) UNIV ROCKEFELLER
                                                                                                                                   WPI; 1995-139598/18.
                                                                                                                                                     N-PSDB; AAQ89340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9620954-A2
   11-MAR-1994;
11-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse STAT4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUL-1996
                                                                                             Darnell JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW03176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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Key Domain Mus sp.

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RESULT 6 AAW03176

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/note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein" 229 13. .229 /note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"
                                                                                                                                             /note= "Wild type Thr substituted with Ala; corresponds to 346 position of Stat-3 protein"
                                                                                                                                                                                   /note= "Wild type Lys substituted with Ala; corresponds to 348 position of Stat-3 protein"
221
                                                                                                                                                                                                                                     /note= "Wild type Arg substituted with Ala; corresponds to 350 position of Stat-3 protein"
                                                       Location/Qualifiers
     therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-226705/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 228 AA;
                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                             WO200116605-A2
                               Mus musculus
                                                                                                                                                                                                                                                                                                      08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                            Zhang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                       Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                    containing 130-358 amino acids of Stati protein. This mutant is obtained by replacing Leu 148 with Ala in Stati protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, colled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                       t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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             'note= "Wild type Leu substituted with Ala; corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                        to 148 position of Stat-3 protein"
213. .229
/note= "Stat3-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NHPTAAVVTEKOOMLEOHLODARKRVODLEOKMKVVENLODDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNNOSVTROKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                         present sequence is mouse Stat3 mutant (L148A) protein fragment
                                                                                                                                                                                                                                                                       Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
99.2%; Score 1163; DB 4; Length 229;
Best Local Similarity 99.1%; Pred. No. 4.4e-99;
Matches 227; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse Stat3 mutant (T346A, K348A, R350A) protein fragment.
                                                                                                                                                                                                                       Darnell JE
                                                                                                                                                                                                                       Wrzeszcynska MH,
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                                                                                                                                                                                                                                                                                                                Claim 66; Page 85; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY72861 standard; protein; 228
                                                                                                                                          30-AUG-2000; 2000WO-US023822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                           (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                      Zhang X, Horvath C,
                                                                                                                                                                                                                                                WPI; 2001-226705/23
Misc-difference 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 229 AA;
                                                                                         WO200116605-A2
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                                                                                                                  08-MAR-2001
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                                       Region
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ID AAY
XX AC AAY
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The present sequence is mouse Stat3 mutant protein fragment containing 130-358 amino acids of Stat3 protein. This mutant is obtained by replacing Thr 346 with Ala, Lys 348 with Ala and Arg 350 with Ala in the Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These indentifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain, linker domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NHPTAAVVTEKQQMLEQHLQD-RKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 GNNOSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VELFRNIAMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1157.5; DB 4; Length
Pred. No. 1.4e-98;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                 Darnell
                                                                                                                                                                                                                                         Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 66; Page 84-85; 86pp; English.
                                                                          31-AUG-1999; 99US-00387418
30-AUG-2000; 2000WO-US023822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.6%;
Matches 228; Conservative
                                                                                                                                                          (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                             Horvath C,
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Length 720;

25-JUL-2002

AAE22055;

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Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, ilposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse ischaemic condition related protein sequence SEQ ID NO:398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VELFRNIAKSAFVVEROPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease.
                                                                                                                                                                                                                                                                                                                                                                     98.7%; Score 1157; DB 5; 98.7%; Pred. No. 7.2e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takahashi Y, Nagata T,
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                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB57164 standard; protein; 769 AA.
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.79
Matches 226; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-034733/04.
N-PSDB; ABI99454.
                                                                                                                                                                                                                                                              Stat3beta protein
                                                                                                                                                                                                                                                                                                                        Sequence 720 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200188188-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating anglogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                                                                                                                        Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypostia; stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; drave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion; Statbeta.
                 180 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 713. .714
/note= "Encoded by ACA CCA TTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 87-89; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dalton W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 713. .714
                                                                                                                                                             AAE22055 standard; protein; 720 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-2001; 2001WO-US028254.
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                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                Human Stat3beta protein.
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WO200220032-A1

Homo

14-MAR-2002

Yu H,

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular

Ishii Y;

N-PSDB; AAD35065

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genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in ABBS7020 to ABBS7347) or by determining the expression profile of a gene group comprising these genes. The expression indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249
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                                                                                                                                                                                                                                                                                                                                                                                                                                            GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 VELFRNIAMKSAFVVERQPCMPWHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                                                                                      Score 1157; DB 5; Length 769;
Pred. No. 7.8e-98;
1; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE22054 standard; protein; 769 AA
                                                                                                                                                                                                                                                                                      98.78;
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                                                                                                                                                                                                                                                                                                                            Matches 226; Conservative
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                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                     Sequence 769 AA;
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                                                                                                                                                                                                                                                                                          Query Match
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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that response. Method involves administering to an individual a compound that conducting a seriative of signal transducer and activator of transcription of Stat3). Modulating angiogenesis is useful for treating or preventing thypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, trisque ischaemia in the lower extremities, infarction, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, coclusion, prenatal or postratory distress syndrome, cardiac arrest, of the necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliotating a symptom of an autoimmune disease such as systemic lupus crythematosus, multiple sclerosis, insulin dependent diabetes mellitus, sypace ornective tissue disease, primary biliary cirrhosis, permicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, vitiligo, comective misculant preventing or treating consertity, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating corrections a predific proliferative and oncogenic disease which includes sarcommas and province or provinced and provinced of architoms of provinced and provi
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                                                                                                             Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ACIGGPPNICLDRIENWITSLAESQLQTRQQIKKLBELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human Stat3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                       Disclosure; Page 83-85; 94pp; English.
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                                                                                                                                                                                                     transcription 3.
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Jove R, Dalton W;

Pardoll D,

Yu H,

10-SEP-2001; 2001WO-US028254 08-SEP-2000; 2000US-0231212P (UYJO) UNIV JOHNS HOPKINS. (UYSF-) UNIV SOUTH FLORIDA.

WO200220032-A1.

Homo

14-MAR-2002

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Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypotals stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis, adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymostis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; disease; ulcerative colitis; sarcoma; carcinoma; degenerative disease; lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 83-85; 94pp; English
                                                                                                                                                                                                                                                                                                                                              Dalton W;
                                                                                                                                                                                                                                                      10-SEP-2001; 2001WO-US028254
                                                                                                                                                                                                                                                                             08-SEP-2000; 2000US-0231212P
                                                                                                                                                                                                                                                                                                                                           Yu H, Pardoll D, Jove R,
                                                                                                                                                                                                                                                                                                      (UYJO ) UNIV JOHNS HOPKINS (UYSF-) UNIV SOUTH FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-362218/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 769 AA;
                                                                                                                                                                                                   WO200220032-A1.
                                                                                                                                                                         Homo sapiens.
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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing, bypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atheroselerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, tissue ischaemia in the lower extremities, infarction, suffocation, prenatal or postnatal oxygen deprivation, suffocation, shock, corolusion, prenatal or postnatal oxygen deprivation, suffocation, shock coronary adult respiratory disease, choking, asphyxia, hypoglycaemia, collusion, prenatal or postnatal cases contain a supplement of an autoimmune response is useful for nitrogen necrosis, proliferative aniquipathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus crythematogus, multiple sclerosis, insulin dependent diabetes mellitus, sjogram's syndrome, scleroderma, polymyosttis, chronic active hepatitis, cancerints tissue disease, primary bilary cirrhosis, pernicious cancemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, ideose, theumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune confinement of disease, theumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune confinement infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, colon carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, the present sequence is human compenial related to angiogenesis regulation
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Matches 226; Conservative
Query Match
Best Local Similarity
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                                                                                                                   1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 60
                                                                                    0; Gaps
                                                Score 1157; DB 5; Length 769;
Pred. No. 7.8e-98;
1; Mismatches 2; Indels C
                                                98.7%;
                                                Query Match
Best Local Similarity 98.73
Matches 226; Conservative
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                                                                                                              ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEBLQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                 250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a mouse acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (IL-6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA library using a polymerase chain reaction product (amplified using primers derived from an IL-6-treated mouse liver peptide) as a probe. ARFF-inhibitors, e.g. antibodies, antisense oligonuclectides or ribozymes, may be used to treat diseases induced by IL-6, e.g. inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQXKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; acute phase response factor; transcription factor; interleukin-6; signal transmission; liver; antibody; antisense; ribozyme; antiinflammatory; antitumor; hypotensive; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New acute phase response factor - for developing inhibitory agents for treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                              GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
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Pred. No. 7.8e-98;
1; Mismatches 2,
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N-PSDB; AAT05619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KISH/) KISHIMOTO T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypertension, etc
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121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater than 5.0 Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New crystals of an N-terminal fragment of a signal transducer and activator of transcription that effectively diffracts x-rays, useful for drug screening and development.
                          250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                       signal transducer and activator of transcription; crystal;
                                                                                       VELFRILMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                     VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
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/label= 3(10) helix of alpha helix
28. .33
/label= Alpha helix 3
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/label= Alpha helix 2
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/label= Alpha helix 4
43. .47
/label= Alpha helix 5
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/label= Alpha helix 8
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|abel= Alpha helix
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                                                                                                                                                                                      AAB12377 standard; peptide; 770
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                                                                                                                                                                                                                                                                                                                                         drug design; murine
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ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
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                                                                  ACIGGPPNI CLDRLENWITSLAESQLOTRQOIKKLBELQQKVSYKGDPIVQHRPMLEBII
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                                                                                                                                                   Score 1157; DB 2; Length 770;
Pred. No. 7.8e-98;
1; Mismatches 2; Indels
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Best Local Similarity 98.7
Matches 226; Conservative
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N-PSDB; AAX29281.
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Matches 226; Conservative 1; Mismatches 2; Indels (
dimensional structure determined for the crystal
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-364-970-3

US-09-364-970-3

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APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REPERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
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US-08-781-890-14
US-09-387-418A-19
US-09-387-418A-19
US-09-387-418A-12
US-09-387-418A-22
US-09-387-418A-23
US-09-387-418A-21
US-09-387-418A-20
US-09-387-418A-20
US-09-387-418A-17
US-09-387-418A-24
US-09-387-418A-17
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US-09-387-418A-17
US-09-387-418A-17
US-09-387-418A-17
US-09-387-418A-17
US-09-387-418A-17
US-09-387-418A-17
US-08-852-091-6
US-08-852-091-6
US-08-852-091-6
US-08-852-051-6
US-08-956-865-6
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Patent No. 6391572
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
                                                                                                                                                                                                                                                                                                                                                                                                       US-09-387-418A-31
; Sequence 31, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
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   ORGANISM: Mus musculus
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IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 ACIGGPPNICLDRLENWITSLABSQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEBRI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFDFNYKTLKSQGMQDLN
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                                                  181 VELFRNIAMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
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                       FKVRLLVKFPEL 229
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Pred. No. 7.1e-99;
0; Mismatches 1;
                       181 VELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOF1
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Sequence 9, Application US/09387418A;
Setent No. 6331572;
GENERAL INFORMATION:
APPLICANT: Areascaynaka, Melissa H
APPLICANT: Horvath, Cut M
APPLICANT: Horvath, Cut M
TITLE OF INVENTION: HYPERACTIONS
TITLE OF INVENTION: METHODS FOR IDENTIFYING;
TITLE OF INVENTION: INTERACTIONS
TITLE REFERENCE: 600-1-253;
CURRENT APPLICATION NUMBER: US/09/387,418A;
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 9
EENCHMARE: PATENTIN Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                           Sequence 14, Application US/09387418A
Patent No. 6391572
GENERAL INFORMATION:
APPLICANT: Chang, Xiaokui
APPLICANT: Wrzesczynska, Melissa H
APPLICANT: Wrzesczynska, Melissa H
APPLICANT: Horvath, James E
TITLE OF INVENTION: INTERFORE E
TITLE OF INVENTION: INTERFCTIONS
FILLS REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILLIO DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 99.6%;
Matches 228; Conservative (
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Best Local Similarity
                                                                                                                                                        US-09-387-418A-14
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LENGTH: 252
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APPLICANT: Alocation US/09387418A
Batent No. 6391572
GENERAL INFORMATION:
APPLICANT: Alocation Statement of the APPLICANT: APPLICANT: APPLICANT: Westerscrynska, Melissa H
APPLICANT: Westerscrynska, Melissa H
APPLICANT: Westerscrynska, Melissa H
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT PAPPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 229
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Pred. No. 6.3e-99;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                           Length 229;
                                                                                                                                                                                                                                                                                                                                         Score 1168; DB 3;
Pred. No. 6.3e-99;
0; Mismatches 1;
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Best Local Similarity 99.6%;
Matches 228; Conservative C
Horvath, Curt M
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.6
Matches 228; Conservative
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US-09-387-418A-18
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APPLICANT:
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Sequence 12, Application US/08852091

Patent No. 588328

GENERAL INFORMATION:
APPLICANT: 21long Wen
APPLICANT: 21long Wen
APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                     250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMBYVQKTLTDEELADWKRRPEI 249
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                                           121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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                                                                                                                               181 VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0, Vel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
FILING APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAMME: Jackbon Esq., David A.
REGISTRATION NUMBER: 26,702,116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKGT NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                            RESULT 7
US-08-852-091-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08369796
Patent No. 5716622
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zilong Wen
APPLICANT: Zilong Wen
APPLICANT: Zhong Zhong
TITLE OP INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OP INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
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                                                                                                                               GNNOSVTROKMOQLEOMLTALDOMRRSIVSELAGLLSAMBYVOKTLTDEELADWKRRPEI 120
                                                                                                                                                        84 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
                                                                                                                                                                                                                    121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                130 NHPTAAVVTEKQOMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                       83
                                                                     24 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                         1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKWKVVENLQDDFDFNYKTLKSQGDMQDLN
Gaps
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                                                                                                                                                                                                                                                                                                        99.7%; Score 1168; DB 1; Length 770; 99.6%; Pred. No. 3e-98;
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ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
GORETING SYSTEM: PC-DOS/MS-DOS
GURENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
FILING DATE: 06-JAN-1995
FILING DATE: 07-MATION:
Ξ,
Mismatches
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0; Mismatches
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 99.0
Matches 228, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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Matches
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                                                                                                                                                                                                                                        US-US-US-124-12
| Sequence 12 Application US/08820754
| Patent No. 597635
| GERRAL INFORMATION:
| APPLICANT: Darnell Jr., James E. APPLICANT: Schindler, Christian W. APPLICANT: Borns, Janong TITLE OF INVENTION: EECPTOR RECOGNITION FACTORS, PROTEIN TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 25
| CORRESPONDENCE ADDRESS: 25
| CORRESPONDENCE ADDRESS: 25
| CORRESPONDENCE ADDRESS: 25
| CORRESPONDENCE ADDRESS: 35
| CORRESPONDENCE ADDRESS: 35
| CORRESPONDENCE ADDRESS: 35
| CORRENT New Jersey
| CONNITY: USA COMPANIES: 14
| COMPUTER READABLE FORM: | COMPANIES: 15 | PACTOR | 
                         181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                   310 VELFRNLMKSAFVVERQPCMPWHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
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Pred. No. 3e-98;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
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Best Local Similarity 99.6%;
Matches 228; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 770 amino acids amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                    US-08-820-754-12
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GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                    190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
                                                                                                      ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                     250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                                                                                                                                                             VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKPPEL 229
                                                                                                                                                                                                                                         310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Pu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECRETOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26,742
TD. 600-1-073 CIP
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CLASSIFICATION
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-MOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
RICH APPLICATION DATA:
APPLICATION UNDERS: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION UNDERS: WO MS93/02569
FILING DATE: 19-MAR-1993
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            US-08-956-652-12
; Sequence 12, Application US/08956652
Patent No. 6013475
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFRENCE/DOCKET NUMBER: 600-1 TELECPHONE: 201 487-5800 TELEPAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 770 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-956-652-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
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us-10-090-185-31.rai

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61 GNNQSVTROKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                              121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                         190 GNNQSVTRQKOQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                           Gaps
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Fatent No. 6124118

GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Wen, Zilong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPENDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                         Score 1168; DB 3; Length 770;
Pred. No. 3e-98;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26,742
ER: 600-1-073 CIP
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATE: 28-NOV-1992
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PELLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FELECOMMUNICATION INFORMATION:
                                                                                           Query Match
Best Local Similarity 99.6%;
Matches 228; Conservative
                             ; MOLECULE TYPE: protein US-08-956-869-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
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         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-948-547-12
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STATE:
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                                                                                                                                                                                                                                                121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                         1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDMQDLN 60
                             Gaps
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                                                                                                                                                                                                                                                                                                                                    181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08956869
Fatent No. 6030608
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Tu, Xtan-Yuan
APPLICANT: Anong Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES. 25
CORRESPONDENCE ADDRESS:
                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,869
FILING DATE:
CLASSIFICATION:
    Pred. No. 3e-98;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/212,185
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Jersev
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INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
Best Local Similarity 99.6%;
Matches 228; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-08-956-869-12
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CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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: USA
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                                                                                                                                                                                                                                                         SEQ ID NO 5
LENGTH: 770
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APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIPERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTI VET: 2.0
                                                                                                                                                                                                                                                                        1 NHPTAAVVTEKOOMLEQHLODARKRVODLEQKMKVVENLODDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                   Score 1168; DB 3; Length 770;
Pred. No. 3e-98;
0; Mismatches 1; Indels
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Pred. No. 3e-98;
0; Mismatches
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Patent No. 6235873
                                                       12:
                                                                                                                                                                                                   99.7%;
TELEFACONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Innear
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                                                                                                                                                                                                 Query Match
Best Local Similarity 99.6
Matches 228; Conservative
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                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-948-547-12
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US-09-364-970-3
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US-09-364-970-5

Sequence 5, Application US/09364970

Sequence 5, Application US/09364970

Sequence 5, Application US/09364970

Sequence 5, Application US/09364970

Sequence 5, Application USSS FOR IDENTIFY INCLUDING TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES

TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES

FILE REFERENCE: 600-1-252

CURRENT APPLICATION NUMBER: US/09/364,970

CURRENT PILING DATE: 199-07-31

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.0
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Sequence 12, Application US/08956653A

Farent No. 6338049

FAPLICANT: Darnell Jr., James E.

APPLICANT: Schindler, Christian W.

APPLICANT: Fu, Xian-Yuan

APPLICANT: Fu, Xian-Yuan

APPLICANT: Application Schindler, Christian W.

TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN

TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES. 34

CORRESPONDENCE ADDRESSE: Alackson

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,653A
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APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.6
Matches 228; Conservative
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ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.7%; Score 1168; DB 3; Length 770;
99.6%; Pred. No. 3e-98;
tive 0; Mismatches 1; Indels
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Barent No. 6605442

GENERAL INFORMATION:

APPLICANT: Darnell Jr., James E.

APPLICANT: Schindler, Christian W.

APPLICANT: Fu, Xian-Yuan

APPLICANT: Wen, Zilong

APPLICANT: Zhong, Zhong

APPLICANT: Zhong, Zhong

TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN

TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                            NAME: Jackson Egg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFK: 201343-1684
TELEK: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 anino acids
TYPE: amino acid
                                                                   PELLING DATE: 19-MAR-1992
PRIOR PAPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
JMBER: US 07/980,498
23-NOV-1992
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STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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Matches 228; Conservative
                            FILING DATE: 23-NOV-1
PRIOR APPLICATION DATA:
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MOLECULE TYPE: protein
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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1168; DB 4; Length 770;
Pred. No. 3e-98;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
AFFLING DATE: 11-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR-1993
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,712,1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: May 25, 2005, 17:47:41
Job time : 29.6534 secs
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INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.6%;
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 770 amino acids
amino acid
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; MOLECULE TYPE: protein
US-08-212-185-12
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May 25, 2005, 17:36:58 ; Search time 100.287 Seconds (without alignments) 763.830 Million cell updates/sec
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/ cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/PCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/PCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1434725 segs, 334507595 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 31, Appl	Sequence 18, Appl	Sequence 28, Appl	Sequence 14, Appl	Sequence 9, Appli	12,	Sequence 12, Appl	Sequence 30, Appl	4,	7	2	8	Sequence 56, Appl
ΩΙ	US-10-090-185-31	US-10-090-185-18	US-10-090-185-28	US-10-090-185-14	US-10-090-185-9	US-09-876-773-12	US-10-639-617-12	US-10-090-185-30	US-10-380-020-4	US-10-380-020-2	US-10-380-020-5	US-10-045-792-8	US-10-038-010-56
ВВ	13	13	13	13	13	11	17	13	15	15	15	14	14
* Query Match Length DB	229	229	229	252	271	770	770	229	720	769	769	770	170
* Query Match	100.0	99.7	99.7	99.7	7.66	7.66	99.7	99.5	98.7	98.7	98.7	98.7	98.7
Score	1172	1168	1168	1168	1168	1168	1168	1163	1157	1157	1157	1157	1157
Result No.	1	7	m	4	S	9	7	80	6	10	11	12	13

19 1 2 1 2 1 2 1 2 2 2 2 2 2 2 2 2 2 2 2	Sequence 19, Appl Sequence 550, Appl Sequence 550, App Sequence 6, Appli Sequence 8, Appli
14 US-10-117-087-2 9 US-09-925-302-780 10 US-09-925-302-780 11 US-09-925-302-780 12 US-10-116-275-349 13 US-10-090-185-29 13 US-10-090-185-15 13 US-10-090-185-15 13 US-10-090-185-12 13 US-10-090-185-22 13 US-10-090-185-22 13 US-10-090-185-24 14 US-10-090-185-24 15 US-09-185-24 16 US-10-090-185-24 17 US-09-185-24 18 US-10-090-185-24 19 US-09-185-24 10 US-09-185-24 11 US-09-185-24 12 US-10-090-185-12 11 US-09-185-12 12 US-10-090-185-12 13 US-10-090-185-12 14 US-10-245-120-2 15 US-09-833-205-2 16 US-10-245-120-2 17 US-10-639-617-6 18 US-10-245-120-1 19 US-09-833-205-2 10 US-09-833-205-2 11 US-09-833-205-2 12 US-10-308-239-352 13 US-10-308-239-352 14 US-10-308-239-352 15 US-10-308-33-30-3	US-10-639-617-4 US-10-639-617-4 US-09-925-297-55 US-09-833-205-6 US-09-876-773-8
77933 77933 77933 7793 7793 7793 7793 7	750 786 749 749
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11157 11157 11157 11152 1152	26299
4 2 3 4 4 4 5 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 4 4 4 1 12 12 4 13

ALIGNMENTS

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Sequence 31, Application US/10090185
Publication No. US20020197647A1
GENERAL INROWATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Wellowska, Wrzeszczynska, Wrzeszc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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100.0%; Pred. No. 7.5e-95;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Mus musculus
JS-10-090-185-31
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LENGTH: 229
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APPLICANT: Wirescacaynska, Melissa H

APPLICANT: Wirescacaynska, Melissa H

APPLICANT: Horvath, Curt M

APPLICANT: Horvath, Curt M

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: 1002-03-04

CURRENT FILING DATE: 2002-03-04

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOSTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
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                                                                                                                                                                                                        1 NHPTAAVVTEKOOMLEOHLODARKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN
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                                                                                                                                                           1; Indels
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Pred. No. 1.9e-94;
                                                                                                            Score 1168; DB 13,
Pred. No. 1.7e-94;
0; Mismatches 1;
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Best Local Similarity 99.6%;
Matches 228; Conservative 0
                                                                                                              99.7%;
                                                                                                                                                           Matches 228; Conservative
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-28
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Best Local Similarity
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TYPE: PRT
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Sequence 28, Application US/10090185

Publication No. US20020197647A1

GENERAL INFORMATION:

APPLICANT: Zhang, Xiaokui

APPLICANT: Areacazynaka, Melissa H

APPLICANT: Horvath, Curt M

APPLICANT: Darnell Jr., James E

TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR FILLE REFRENCE: 600-1-253

CURRENT FILLING DATE: 2002-03-04

PRIOR FILLING DATE: 1999-08-31

FUNDER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                             APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Curk
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILLE REPERENCE: 600-1-23
FILLE REPERENCE: 600-1-23
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.0
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                                121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLBELQQKVSYKGDPIVQHRPMLEERI 180
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Pred. No. 1.7e-94;
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                                                                                                                                                                                                                                                Sequence 18, Application US/10090185; Publication No. US20020197647A1; GENERAL INFORMATION:
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US-10-090-185-18
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Best Local Similarity
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120

RESULT 5 US-10-090-185-9

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130 NHPTAAVVTEKQQMLEQHLQDVKKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLM 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                       FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: WO 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESQ., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.6%; Pred. No. 7.9e-94;
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Publication No. US20050079543A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
FW. Xian-Yuan
Wen, Zilong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 770 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Klauber
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COMPUTER READABLE FORM:
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STATE: New Jersey
COUNTRY: USA
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Matches 228; Conservative
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US-10-639-617-12
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                                                                                          APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Barnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR ITILE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT PILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR APPLICATION ONS: 43
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 GNNQSVTRQKWQQLEQMLTALDQWRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
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TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1168; DB 13
Pred. No. 2.1e-94;
0; Mismatches 1
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ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09876773
Publication No. US20040058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Fu, Xian-Yuan
Wen, Zilong
Sequence 9, Application US/10090185 Publication No. US20020197647A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.7%;
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PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.6
Matches 228; Conservative
                                                                          APPLICANT: Zhang, Xiaokui
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US-09-876-773-12
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LENGTH: 271
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Sequence 4, Application US/10380020
; Beducation No. US20040052762A1
; GENERAL INFORMATION:
    APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Dalton, Willian
; TITLE OF INVENTION Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR PILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 4
; SEQ ID NO 4
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                                                                                                                                                                                                                             1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 60
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                                                                                                                                                                                                 1 NHPTAAVVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                    Length 229;
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Pred. No. 6.7e-93;
1; Mismatches 2; Indels 0
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                                                                                                                                                Indels
                                                                                               Score 1163; DB 13;
Pred. No. 4.6e-94;
0; Mismatches 2;
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; Publication No. US20040052762A1
                                                                                                  99.2%;
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Best Local Similarity 98.7%;
Matches 226; Conservative
                                                                                               Query Match
Best Local Similarity 99.1
Matches 227; Conservative
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo Sapiens
                            ; OKGANISM. ....
US-10-090-185-30
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US-10-380-020-2
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; Sequence 30. Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR F
; TITLE OF INVENTION: MYBER US/10/090,185
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT PILING DATE: 2002-03-04
; PRIOR PILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NOS: 43
; SEQ ID NO 30
; SEQ ID NO 30
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                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFRAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 99.7%; Score 1168; DB 17
Best Local Similarity 99.6%; Pred. No. 7.9e-94;
Matches 228; Conservative 0; Mismatches 1
                                                                                                            APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY AGENT INFORMATION:
               APPLICATION NUMBER: US/10/639,617
FILING DATE: 12-Aug-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12
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SEQUENCE CHARACTERISTICS:
                                                                                          PRIOR APPLICATION DATA:
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121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
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                                                                         250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
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TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF
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Pred. No. 7.3e-93;
1; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-OCC-2001
CLASSIFICATION & CURROWN>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/012,710
FILING DATE: CURROWN>
ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REFERENCE/COCKET NUMBER: 26,742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                  Moarefi, Ismail
Darnell, Jr., James E.
Kuriyan, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                        ; Sequence 8, Application US/10045792; Publication No. US20030003563A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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Best Local Similarity 98.7%;
Matches 226; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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ULE TYPE: protein
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                                                         APPLICANT: JOVE, Richard
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stata Agonists and Antagonists and Therapeutic Uses Thereof
FITLE OF INVENTION: Stata Agonists and Antagonists and Therapeutic Uses Thereof
FILE REPRENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
CURRENT APPLICATION NUMBER: 60/231,212
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10380020
Publication No. US20040052762A1
GENERAL INFORMATION:
APPLICANT:
Dalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof FILE REFERENCE: 10873-009-999
CURRENT FILING DATE: 2003-03-07
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
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Pred. No. 7.3e-93;
1; Mismatches 2;
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SOFTWARE: PatentIn version 3.0
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Best Local Similarity 98.7
Matches 226; Conservative
GENERAL INFORMATION:
APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo Sapiens
US-10-380-020-2
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US-10-380-020-5
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                                           APPLICANT:
APPLICANT:
APPLICANT:
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ORGANISM: Human
        US-10-117-087-2
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121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                    250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPWLEERI 309
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US-10-038-010-56
; Sequence 56, Application US/10038010
; Publication No. US20030040089A1.
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFRENCE: B4767.
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR PELING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
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                                                                            181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
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Pred. No. 7.3e-93;
1; Mismatches 2; Indels 0
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Publication No. US20030166854A1

GENERAL INFORMATION:
APPLICANT: SERLUPI-CRESCENZI, Ottaviano
FILE SERLORICES SERLUPI-Z
CURRENT APPLICATION: ALLELIC VARIANTS OF HUMAN STAT3
FILE REFERENCE: SERLUPI-2
CURRENT PILING DATE: 2002-04-08
PRIOR PILING DATE: 2002-04-08
PRIOR FILING DATE: 2000-03-19
NUMBER OF SEQ 1D NOS: 19
SOFTWARE: Patentin version 3.0
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US-10-038-010-56
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Best Local Similarity 98.7%;
Matches 226; Conservative 1
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US-10-117-087-2
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LENGTH: 770
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                                                                                                                                                     130 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN 189
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Length 770;
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| Sequence 780, Application US/09925302
| Patent No. US20020044941A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies |
| FILE REFERENCE: PA104
| CURRENT APPLICATION NUMBER: US/09/925,302
| CURRENT FILING DATE: 2001-08-10
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 8966
| SOFTWARE: Patentin Ver. 2.0
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Pred. No. 7.6e-93;
1; Mismatches 2; Indels
                                                     Indels
Score 1157; DB 14
Pred. No. 7.3e-93;
1; Mismatches 2
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  98.78;
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Best Local Similarity 98.73
Matches 226; Conservative
Query Match
Best Local Similarity 98.77
Matches 226; Conservative
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ORGANISM: Homo sapiens
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US-09-925-302-780
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 25, 2005, 17:24:07 ; Search time 21.6038 Seconds (without alignments) 1019.898 Million cell updates/sec

US-10-090-185-31 1172 Perfect score:

1 NHPTAAVVTEKQQMLEQHLQ......IKTGVQFTTKVRLLVKFPEL 229 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ISGF3 p91-related	DNA-binding protei	interferon-depende	gamma-interferon a	interferon alpha-i	mammary gland fact	mammary gland fact	transcription acti		interleukin-4-indu	DNA-Binding Protei	chromosome segrega	hypothetical profe	conserved hypothet	hypothetical prote	myosin heavy chain	tpr protein - huma	M protein - Helico	median body protei	myosin heavy chain	myosin heavy chain	microtubule bindin	myosin heavy chain	nuclear/mitotic ap	epimorphin - mouse	myosin heavy chain	tropomyosin 2, ske	hypothetical prote	_
SUMMARIES	ID	149508	A54444	A46159	A56047	A46160	149274	S54772	G02317	S55527	A54740	157557	AE1947	G72593	A70387	T27075	A27224	S33124	C64527	S33821	806117	S21801	T13030	B43402	T30336	S51193	A59252	S24401	T27055	T51505
	Length DB	770 2		739 2		•				794 2				533 2		1166 2							• •	2007 1	•			284 2		m
م	Query Match Le	98.7	98.3	44.7	Э.	۲.	22.9	22.9	22.4	20.2	10.8	10.7		10.4	4.	۳.	٥.	٥.	₽.	9.6	۲.	9.	9.	9.	9.	9.		9.5		9.5
	Score	1157	1152	523.5	508	322	268.5	268.5	262.5	237	127	125.5	122.5	122	122	120.5	116.5	116.5	114.5	114.5	113.5	113	112.5	112.5	112.5	112	112	111	111	111
	Result No.	-	7	e	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

A54444 DNA-binding protein APRF - human

RESULT 2

hypothetical prote	chromosome segrega	interaptin - slime	hypothetical prote	microtubule bindin	hypothetical prote	exonuclease (EC 3.	hypothetical coile	centrosome associa	myosin heavy chain	364K Golgi complex	SCP1 protein - rat	myosin heavy chain	myosin heavy chain	desmoplakin I - hu	myosin heavy chain
T24806	G83960	T14867	T43448	H90279	AC1814	BVECSC	T38077	T08621	A33977	JC5837	S28061	A59287	A47297	A38194	833068
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1164	1188	1738	434	464	727	1048	1957	2442	1959	3187	946	1940	1992	2677	527
9.5	9.5	9.4	9.3	9.3	9.3	9.3	9.3	9.3	9.3	9.3	9.3	9.3	9.3	9.5	9.5
111	111	110.5	109.5	109.5	109.5	109.5	109.5	109.5	109	109	108.5	108.5	108.5	108	107.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-ul-1996 #sequence_revision 02-ul-1996 #text_change 09-Jul-2004
C;Acresion: 149509
R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sur Call 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: 149508
A;Accession: 149508
A;Residues: 1-770 cRES-A;Cross-references: Unbranch A;Residues: 1-770 cRES-A;Cross-references: Unbranch JE.; Levy, D.E.
J. Biol. Chem. 269, 24391-24395, 1994
A;Accession: 149009
A;Acteus: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 149009
A;Accession: 149009
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-393, WW, 395-700, 702-770 cRES-A;Cross-references: EMBL:U08378; NID:9473889; PIDN:AAA56668.1; PID:9473890
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ISGF3 p91-related transcription factor - mouse
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A;Molecule type: DNA
A;Residues: 1-851 <XAN>
A;Residues: 1-851 <XAN>
A;Cross-references: EMBL:U18671; NID:g1293919; PIDN:AAA98760.1; PID:g1293920
A;Cross-references: EMBL:U18671; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in
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     250 GPPNACLDOLQ----
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                   C,Accession: A5444
C;Accession: A5444
C;Accession: A5444
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C;Accession: A5444
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C;Accession: A54444
C;Accession: A54444
C;Accession: A54444
C;Accession: A54444; MUID:94208062; PMID:7512451
A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: A54444
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPROT:P40763; GB:L29277; NID:g475788; PID:g475789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: A46159
R;Schindler, C.; Fu, X.Y.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa ISGA;Accession: A46159; MUID:92366557; PMID:1502203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEIACIG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPPNICLDRLENWITSLAESQLOTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NHPTAAVVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 60
Species: Homo sapiens (man)
Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Homo sapiens (man)
Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNNOSVTROKMOQLEOMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 GNNQSVIRQKWQQLEQMLTALDQMRRSIVSELAGLLAGAMEYVQKTLIDBELADWKRRQQI
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                                                                                                                                                                                                                                                                                                                                   A,Gene: GDB.STAT3; APRF
A,Cross-references: GDB.358950
A,Map position: 17421-17421
C,Superfamily: human signal transducer and transcription activator STATSA
C,Keywords: DNA binding; transcription factor
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A;Molecule type: nucleic acid; protein
A;Molecule type: nucleic acid; protein
A;Residues: 1-739 <SCH>
A;Cross-references: UNIPROT: P42224
A;Cross-references: UNIPROT: P42224
A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator STAT5A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
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Best Local Similarity 98.3%; Pred. No. 5.9e-69;
Matches 225; Conservative 1; Mismatches 3;
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44.7%; Score 523.5; DB 2
Best Local Similarity 45.8%; Pred. No. 2.6e-27;
Matches 103; Conservative 49; Mismatches 60
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Cispecies: Mus musculus (house mouse)
Cispecies: Jo-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
Cistoresion: A56047
Rivamamoto, K.; Ouelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, Mol. Cell. Biol. 14, 434-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in e A;Reference number: A56047
A;Accession: A56047
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P42228; GB:U09351; NID:g509502; PIDN:AAA19692.1; PID:g50950 C;Superfamily: human signal transducer and transcription activator STATSA C;Keywords: DNA binding; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interferon alpha-induced transcription activator ISGF-3, 113K chain - human NyAlternate names: stat2 protein
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46160; S71908; S53873
R;Fu, X.Y; Schindler, C.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. US.A. 89, 7840-7843, 1992
R;Fu X.Y; Schindler, C.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator A;Reference number: A46160; MUID:92366558; PMID:1502204
A;Accession: A46160
A;Accession: A;Residues: Decliminary; not compared with conceptual translation
A;Molecule type: mRNA; protein
A;Note: sequence extracted from NCBI backbone (NCBIP:110820)
B;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell, J.E.
Submitted to the EMBL Data Library, December 1994
A;Reference number: S71908
A;Accession: S71908
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-- OVROOLKKLEELEOKYTYEHDPITKNKOVLWDRTFSLF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 PPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 VTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKS--QGDMQDLNGNNQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 VTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEIACIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 748;
                                                                                                                            gamma-interferon activation site-binding protein Stat4 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66; Indels
                                                                            185 RNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.3%; Score 508; DB 2; 45.5%; Pred. No. 2.8e-26;
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A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:Z48538; NID:g758633; PIDN:CAA8 R;Liu, X.; Robinson, G.W.; Goullleux, F.; Groner, B.; Hennighausen, L. Prod. Sci. U.S.A. 92; 8831-8835, 1995 A;Fitle: Cloning and expression of Stats and an additional homologue (Stat5b) involved A;Reference number: 149273; MUID:96004632; PMID:7568026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleuki A;Reference number: S54772; MUID:95237198; PMID:7720707 A;Accession: S54772 A;Accession: S54772 A;Status: preliminary; nucleic acid sequence not shown
                                                                        254 QWKRRQQLAGNGGPPEGSLDVLQSWCEKLAEIIWQNRQQIRRAEHLCQQLPIPG-PVEEM 312
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                                                                                                                                                                                                       194 PQERMSRETALQQKQVSLETWLQREAQTLQQYRVELAEKHQKTLQLLRKQQTIILDDELI 253
                                                                                                                                                                                                                                                              113 DWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQH 172
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G02317
transcription activator stat5A - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNY-KTLKSQGDMQDLNGNN
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                                                                                                                                                                                                                                                                                                                                                                                                         313 LAEVNATITDIISALVTSTFIIEKQP------PQVLKTQTKFAATVRLLV 356
                                                                                                                                                                                                                                                                                                                                                                      173 RPMLBERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLV 224
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; Pred. No. 2.2e-10;
41; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-793 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: stat5 protein
C;Species: Mus musculus (house mouse)
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A; Residues: 1-793 < MUI>
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A;Residues: 1-786 <RES.
A;Rolecule type: mRNA
A;Residues: 1-786 <RES.
A;Cross=refecences: UNIPROT:09JXM1; EMBL:U21110; NID:9747973; PIDN:AACS2
R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
BMBO J. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
A;Reference number: S54772; MUID:95237198; PMID:7720707
A;Reference number: S54772; MUID:95237198; PMID:7720707
A;Residues: I-432, E',434-786 <MUI>A;Residues: S84727, By MID:95246733; PMID:7537213
A;Recence number: S54727
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.Alternate names: STATS protein homolog p80
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: O2-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149274; S54727
R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved A;Reference number: 149273; MUD:96004632; PMID:7568026
A,Reference number: S53873; MUID:95192056; PMID:7885841
A,Accession: S53873
A,Status: nucleic acid sequence not shown
A,Status: nucleic acid sequence not shown
A,Rolecule type: DNA
A,Rossereferences: EMBL:018671
C,Genetics:
A,Gene: stat2
A,Genetics:
A,Genetics:
A,Genetics:
C,Superfamily: human signal transducer and transcription activator STAT5A
C,Keywords: signal transduction; transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :| :| | : | | : | 138 VESQQHEIESRILDLRAMMEKLVKSISQLKDQQDVFCFRYK-1QAKGKTPSLDPH--QTK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEIACIGGPP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 DHGLEQLETWFTAGAKLLFHLRQLLKELKGLSCLVSYQDDPLTKGVDLRNAQVTELLQRL 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 VTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVT
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                                                                                                                                                                                                                                                                                                                                            Score 322; DB 2; Length 851;
Pred. No. 6.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 MKSAFVVEROPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPE 228
                                                                                                                                                                                                                                                                                                                                                                                                   90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                   51; Mismatches
                                                                                                                                                                                                                                                                                                                                      Query Match 27.5%; Score 322; Best Local Similarity 33.5%; Pred. No. 6 Matches 74; Conservative 51; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Residues: 1-432,'E',434-786 <AZA>
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Best Local Similarity
Matches 71; Conserv
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DNA-Binding Protein and transcription factor - mouse C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C; Accession: 157557
R; Quelle, F.W.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M.; Clev Mol. Cell. Biol. 15, 3336-3343, 1995
A; Title: Cloning of murine Stat6 and human Stat6, Stat proteins that are tyrosine phosp A; Reference number: 157557; MUID:95280934; PMID:7760829
A; Accession: 157557
A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: UNIPROT:P52633; GB:L47650; NID:gL008876; PIDN:AAA79006.1; PID:g1008
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Species: 128-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: A54740
R;Hou, J.; Schindler, U.; Henzel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
Science 265, 1701-1706, 1994
A;Title: An interleukin-4-induced transcription factor: IL-4 stat.
A;Reference number: A54740; MUID:94367369; PMID:8085155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 TDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 PLKLVAT----FROILOGKKKAV-----MEQFRHLPMPFHWKQEELKFKTGLRRLOHR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 NQSV--TRQKMQQ------LEQML-----TALDQMRRSIVSELAGLLSAMEYVQKTL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 D----LNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMBYVQKTLTDEELA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 GELEPKTRASLIGRLDEVLRTLVTSCFLVEKQP-----PQVLKTQTKFQAGVRFLL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 DPI-VQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 BKKAVIEBFRHLPGPFHRKQEELKFTTPLGRLHHRVRETRLLRESLHLGPKT--GQVSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PTAAVVTEKOOMLEQHIQDARKRVODLEQKMKVVENLQDDFDFNYKTLKSQGDMODLNGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Residues: 1-848 <HOU>
A,Zross-references: UNIPROT:P42226
C,Superfamily: human signal transducer and transcription activator STATSA
C,Keywords: DNA binding; transcription regulation
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C;Superfamily: human signal transducer and transcription activator STAT5A
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                                   176 LEERIVELFRNIMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLV 224
                                                                      316 VNATITDIISALVTSTFIIEKQP------PQVLKTQTKFAATVRLLV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 837;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A54740
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 127; DB 2;
Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    th 10.8%; Score 127; DB Similarity 24.7%; Pred. No. 0.58 59; Conservative 37; Mismatches
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Best Local Similarity
Matches 59; Conserval
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A;Residues: 1-837 <RES>
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A,Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:g1151169; PIDN:AAB06589.1; PID:g115
C;Superfamily: human signal transducer and transcription activator STAT5A
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A, Residues: 1-794 < WAKA.

A, Residues: 1-794 < WAKA.

A, Cross-references: UNIPROT: P42231; EMBL: X78428; NID: 9602354; PIDN: CAA55191.1; PID: 96023

A, Note: this is a revision to the sequence from reference $44353

R, Wakao, H.; Gouilleux, F.; Groner, B.

EMBO J. 13, 2182-2191, 1994

A, Title: Manmary gland factor (MGF) is a novel member of the cytokine regulated transcri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S5522; S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
BEMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regula
A;Reference number: S55527; MUID:95188889; PMID:7882987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 NGNNQSVTRQKMQQLEQML----TALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----QSVIRQKWQQLEQML----TALDQMRRSIVSELAGLLSAMEYVQXTLTDEELADWK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPM 175
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                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: mRNA
A,Residues: 1-716, RHLHGPGSLPSR',729,'P',731,'ASL' <WAW>
A,Cross-references: EMBL:X78428
A,Note: this sequence has been revised in reference S55527
C,Superfamily: human signal transducer and transcription activator STATSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 LEERIVELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLV 224
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                                                                                                                                                                                                                                                                                                                                              Length 794;
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                                                                                                                                                                                                                                                                                                                                           22.4%; Score 262.5; DB 2; Length 79 30.1%; Pred. No. 5.6e-10; rative 42; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99; Indels
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20.2%; Score 237; DB 2;
Best Local Similarity 29.3%; Pred. No. 2.8e-08;
Matches 67; Conservative 41; Mismatches 99;
                                                      submitted to the EMBL Data Library, December 1995 Afferfence number: H01043 Afference number: H01043 Afferesion: G02317 Afferesion: G02317 Afference: preliminary; translated from GB/EMBL/DDBJ Afferens: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                        69; Conservative
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 69; Conserv
C; Accession: G02317
R; Lin, J.
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: A:Gene: APB1216 -GTVGDLETTO-PLVLLRIQ 202		224 OY 297 OY OY	Db 379 LAEAQASEDLATRIDOVA-STLOQUOGRILATAEESLAGALTEDLASLOAEVETLOGSIVE 437 ain PCC 7120)	lange 09-Jul-2004 Qy 165 KGDPIVQHRPMLEBRIVE 182 Co, S.; Watanabe, A.; Iriguchi ida, M.; Yasuda, M.; Tabata, S Db 486ELRTQLDEXTRE 497	RESULT 14 A70387 conserved hypothetical protein aq_1006 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004 C;Acter 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004		1 52	894 111 954	2		Db 282 Qy 114 Db 342 Takah Qy 174 J.; ½ Db 394	NESULT 15 T27075 T27075 hypothetical protein Y51A2D.16 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #equence revision 15-Oct-1999
—ნ ¦	DWKRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLE-ELQQKVSYKGDPIVQ ::	HRPMLEBRIVELFRIMKASPYVEROPCMPHIPDRPLVIKTGVOFTTKVELV HRPMLEBRIVELFRIMKASPYVEROPCMPHIPDRPLVIKTGVOFTTKVELLV 	in [imported] - Nostoc sp. (e 20 C 7120 is a synonym of Anabae	C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 C;Accession: AE1947 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, NDA Res. R. 205-213, 2001	Mar Ness. 9, 203-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AE1947 A;Accession: AE1947 A;Coteserian pre: DNA A;Residues: 1-1208 «KUR» A;Cross-references: UNIRROT:Q8YXT3; GB:BA000019; PIDN:BAB73085.1; PID:g17130474; GSPDB:G	A;Genetics: A;Gene: alr1128 C;Superfamily: chromosome segregation protein SMC1 Ouery Match	뭐 1	35 ATINIQEQUIQUETAFREAEQRIKANLENGOQRICERIQEAQQRITEYQTQCTTCTEAIN 53 QGDMQDLNGNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMBYVQKTLTDEEL 51	112 ADWKRRPEIACIGGPPNICLDRLENWITSLAESOLGTRQI 15	153KKLEELQOKV-SYKGDPIVQHPPMLEERIVELFRNIMKSAF 192 1914 ALEEVERTOKRLEELSQKLOFLEGERTELLLRI-ENFTTLRQIAF 105	RESULT 13 G72593 hypothetical protein APE1216 - Aeropyrum pernix (strain K1) C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004 C;Accession: G72593 R;Kawarabayasi, Y:; Hino, Y:; Horikawa, H.; Yamazaki, S:; Haikawa, Y:; Jin-no, K.; awa, H.; Takamiya, M.; Masuda, S.; Punahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,	NA Res. 6, 83-101, 1999 Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchae Reference number: A72450; MUID:99310339; PMID:10382966 Accession: G72593 Status: preliminary Molecule type: DNA Residues: 1-533 «KAW»

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A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Acatus: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Acasicus: 1-1166 < WIL>
A;Cross-references: EMBL:AL021497; PIDN:CAA16403.1; GSPDB:GN00023; CESP:Y51A2D.16
A;Experimental source: clone Y51A2D
A;Experimental source: clone Y51A2D
A;Gene: CESP:Y51A2D.16
A;Gene: CESP:Y51A2D.16
A;Gene: CESP:Y51A2D.16
A;Gene: CESP:Y51A2D.16
A;Gene: CESP:Y51A2D.16
A;Acasicus: 17/3; 45/1; 76/2; 156/3; 240/2; 288/2; 594/2; 657/3; 756/3; 798/2; 900/3; 948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 FDFNYKTLKSQGDMQDLNGNNQSVTRQXMQQLEQMLTALDQMRRSIVSELAGLLSAMEY- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 538 GANFEKINNDDELIDNIDDIMMNALVAVKRERDDLRIQGNQQIQELHDLKRDIEKLRRSE 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 --CLDRLENWITSLAESQLQTRQQI----KKLEELQQKVSYKGDPIVQHRPMLEERIVEL 183
                                                                                                                                                                                                                                                                                                                                                                                                                       1 NHPTAAVVTEKQ----QMLEQHLQD------ARKRVQDLEQKMKVVENLQDD 42
                                                                                                                                                                                                                                                                                                                                                          72; Indels 73; Gaps
                                                                                                                                                                                                                                                                                                Query Match
10.3%; Score 120.5; DB 2; Length 1166;
Best Local Similarity 21.4%; Pred. No. 2.3;
Matches 52; Conservative 46; Mismatches 72; Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: May 25, 2005, 17:45:30 Job time : 22.6038 secs
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May 25, 2005, 17:15:30 ; Search time 95.284 Seconds (without alignments) 1230.701 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                        OM protein - protein search, using sw model
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US-10-090-185-31 1172 1 NHPTAAVVTEKQQMLEQHLG.....IKTGVQFTTKVRLLVKFPEL 229 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched: Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P40763 homo sapien	P42227 mus musculu	P52631 rattus norv	P61635 bos taurus	Q6dv79 gallus gall		Q7zxk3 xenopus lae	Q7zt85 brachydanio		Q6gue7 oryzias lat		093599 brachydanio		013133 oncorhynchu	O9n145 macaca mula	Q8jgn0 xenopus lae	Q6p6q7 rattus norv	Q9qxk0 rattus norv	Q8c497 mus musculu	Q99k94 mus musculu	Q8c3v4 mus musculu	Q9d323 mus musculu	Q8c8m3 mus musculu	P42224 homo sapien	Q68d00 homo sapien	Q764m5 sus scrofa	P42225 mus musculu	O13131 oncorhynchu	Q8jfu8 brachydanio	Q704w6 bos taurus	093598 brachydanio
SUMMARIES	ID	STA3 HUMAN	STA3 MOUSE	STA3_RAT	STA3_BOVIN	Q6DV79	O9PVX8	Q7ZXK3	Q7ZTS5	Q6DVF3	Q6GUE7	Q6NV46	093599	Q90Y16	013133	Q9N145	Q8JGN0	Q6P6Q7	Q9QXK0	Q8C497	Q99K94	Q8C3V4	Q9D323	QBCBM3	STA1 HUMAN	Q68D00	Q764M5	STA1 MOUSE	013131	QBJFUB	Q704W6	093598
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مد	Query	98.7	98.7	98.5	98.1	96.6	93.8	93.5	86.3	86.3	86.3	86.3	86.3	84.2	83.4	56.0	49.1	48.9	48.9	48.7	48.6	48.6	48.6	48.6	48.5	48.5	48.5	48.0	46.1	45.5	45.4	45.4
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32	33	34	32	36	37	38	39	40	41	42	43	44	45	,

ALIGNMENTS

RESULT STA3_H ID_S	JT 1 HUMAN STA3_HUMAN S
정단	916; Q9BW54; (Rel. 31, Creat
i d	44, Last sequence update) 45, Last annotation update)
0 0 0 0	Signal transducer and activator of transcription 3 (Acute-phase response factor).
8	Name=STAT3; Synonyms=APRF;
S 0	Homo sapiens (Human). Eukarvota: Metazoa: Chordata: Craniata: Vertehrata: Euteleostomi:
88	alia, Eutheria, Primates;
X S	NCBI_TaxID=9606;
RP	SEQUENCE FROM N.A. (ISOFORM 1).
R K	TISSUE=Placenta; MEDLINE=94208062: PubMed=7512451: DOI=10 1016/0092-8674(94)90235-6:
\$	Akira S., Nishio Y., Inoue M., Wang XJ., Wei S., Matsusaka T.,
S E	Yoshida K., Sudo T., Naruto M., Kishimoto T.; "Molecular cloning of Appe a novel Ten. rimulated cons factor 2 nol-
Z E	related transcription factor involved in the qp130-mediated signaling
RT	.pathway:";
7 2	(211 77:63-71(1994).
ž 2	SEQUENCE PROM N.A. (ISOFORM 1).
ă	0560; DOI=10.1016/S0378-1119(98)
Į.	Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;
2 E	"Highly conserved amino-acid sequence between murine STAT3 and a
R 1	revised numan SIAI3 sequence."; Gene 213:119-124(1998).
Z.	[3]
RP	SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.
8 2	Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
\$ £	.kajkumar N., 11 Q., Nickerson D.A.; "SeattlesNPs: NHLBI HL66682 program for genomic applications: IW-
RT	FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
R.	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
R. P.	SEQUENCE FROM N.A. (ISOFORMS 1 AND DEL-701).
S.C.	
2 6	MEDLINE=2238825/; PUDMED=124//932; DOI=10.10/3/pha8.242603899; Stranghory D I. Reinsold P & Gronse I. H. Derse I G
§ §	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
æ	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Z G	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
5 5	Stableton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
æ	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Z Z	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rocak S. McRwan D.I. McKornan K.I. Malek I A. Gunaratne D.H
2 2	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Z G	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Ş	Falley U., HELLON B., Nettellian F., Madan A., NOLLIYUED C., Cameries A.,

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RESULT
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GO:0005634; C:nucleus; TAS.
GO:0005602; F:hematopoietin/interferon-class (D200-domain. . .; TAS.
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pubmed=1173073 DI=10.1074/jbc.M111486200;

Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;

"Functional interaction of STAT3 transcription factor with the coactivator NoA/SRCIa.";

J. Biol. Chem. 277:8004-8011(2002)

-!- FUNCTION: Transcription factor that binds to the interleukin-6

(IL-6) responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOId=P40763-2; Sequence=VSP 010474;
TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.; "Requirement of serine phosphorylation for formation of STAT-promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          muscle, kidney and pancreas.
PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTP,
ILF, CSF-1, EGF, PFGF, IFN-and OSM. Serine phosphorylation
is important for the formation of stable DNA-binding STAT3
                                                                                                                                                                                                                                                                                     Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homodimers and maximal transcriptional activity.
-!- SIMILARITY: Belongs to the transcription factor STAT family.
-!- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P40763-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                        [6]
PHOSPHORYLATION ON SERINE.
MEDLINE=95215843; PubMed=7701321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ012463; CAA10032.1; -. EMBL; AY572796; AAS66986.1; -.
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                                                                                                                                                                                                                                   SEQUENCE OF 564-704 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L29277; AAA58374.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 267:1990-1994(1995)
[7]
                                                                                                                                                           and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T01493; -.
Genew; HGNC:11364; STAT3.
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                                                                                                                                                                                                                                                           TISSUE=Liver;
                                                                                                                                                                                                                                                                                   Della Pietra
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ACIGGPPNICLDRIENWITSLAESQLOTROOIKKLEELQOKVSYKGDPIVQHRPMLEERI 180
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                                                          . .; TAS.
                                                                                                                                                                                                                                                                                                                       similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 ACIGGPPNICLDRLENWITSLASSQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 NHPTAAVVTEKQOMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                 Pfam; PF0017; SH2; 1.
Pfam; PF01017; SH2; 1.
Pfam; PF0264; STAT_alpha; 1.
Pfam; PF02865; STAT_int; 1.
PROSTTE; PS50001; SH2; 1.1
Activator; Alternative splicing; DNA-binding; Nuclear protein;
Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last amnotation update)
5ignal transducer and activator of transcription 3 (Acute-phase
                                                          transcription from P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.7%; Score 1157; DB 1; Length 770; 98.7%; Pred. No. 2.9e-65; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                   Phosphotyrosine (by JAK) (By Phosphoserine (By similarity) Missing (in isoform Del-701). /FTId=VSP_010474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 Q -> H (in Ref. 1).
460 P -> S (in Ref. 1).
548 K -> N (in Ref. 1).
561 F -> Y (in Ref. 1).
667 V -> L (in Ref. 1).
730 Y T -> A (in Ref. 1).
730 Y T -> A (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                         7 - X (in dbSNP:1803125)
YFTIG=VAR_018683.
GO, GO:0003700; F:transcription factor activity; TAS.
GO; GG:0006928; P:cell motility; TAS.
GO; GO:000122; P:GA-STAT cascade; TAS.
GO; GO:000122; P:negative regulation of transcriptio
GO; GO:0007399; P:neurogenesis; TAS.
GO; GO:007165; P:signal transduction; TAS.
InterPro; IPR0008967; PS3_like_DNA_bnd.
InterPro; IPR0008969; SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        018679
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Name=Stat3; Synonyms=Aprf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                            701
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ID STA3 MOUSE
AC P42227;
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STRAIN=FVBN/N, TISSUE=Mammary gland;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Rauberg R.D., Colline F.S., Magner L., Shenmen C.M., Schuler G.D.,

A Ratechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A platchenk L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L.,

B topleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rotriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain, MEDLINESSO.4185, PubMed=7523373; MEDLINESSO.4185; PubMed=7523373; Raz R., Durbin J.E., Levy D.E.; "Acute phase response factor and additional members of the interferonstituted gene factor 3 family integrate diverse signals from cytokines, interferons, and growth factors."; J. Biol. Chem. 269:24391-24395 (1994).
                                                                                                                                                                                                             Zhong Z., Wen Z., Darnell J.E. Jr., "Stat3: a STAT family member activated by tyrosine phosphorylation in "Stat3: e spidermal growth factor and interleukin-6."; science 264:95-98(1994).
Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T., Yoshida K., Sudo T., Naruto M., Kishimoto T.; "Molecular cloning of APRF, a novel IRF-stimulated gene factor 3 p91-related transcription factor involved in the gpl30-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM STAT3B).
STRAIN=BALB/c, and CS7BL/6; TISSUE=Liver;
MEDLINE=96016116; PubMed=7568080;
Schaefer T.S., Sanders L.K., Nathans D.;
"Cooperative transcriptional activity of Jun and Stat3 beta, a short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Structure of the mouse stat 3/5 locus: evolution from Drosophila to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CS7BL/6J, and NOD/LtJ;
Davoodi-Semiromi A., She J.-X.;
A mutant StatSb with weaker DNA binding defines a key defective pathway in non-obese diabetic (NOD) mice.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129/SvJ;
PubMed=11161808; DOI=10.1006/geno.2000.6433;
Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T.,
Dewar K., Hennighausen L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
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                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM STAT3A).
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                                                                                                                                                                                           MEDLINE=94188718; PubMed=8140422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zebrafish to mouse.";
                                                                                                           Cell 77:63-71(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Form of Stat3.";
                                                                                                                                                                           rissum=Thymus;
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NR WEDLING=9515405; pubmed=9514024; DOI=10.1016/0092-8674(95)903111-9; NR WEDLING=9515405; pubmed=9514024; DOI=10.1016/0092-8674(95)903111-9; NR WEDLING=9515405; pubmed=951405; pubmed=951404; pubmed=951401; pubmed=95
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Similarity
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hes 225;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                   TTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
FDMDLTSECAȚSPM -> FIDAVWK (in isoform
                                                                                                  Phosphotyrosine (by JAK) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]
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                                                                                                                                                                                              Missing In isoform Del-701).
/FTId=VSP 010475.
S->A: Decreased transcriptional activation.
E -> K (in Ref. 2).
E -> T (in Ref. 2 and 4).
M -> I (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 770;
               PROSITE; PS50001; SH2; 1.
3D-structure; Activator; Acute phase; Alternative splicing;
Direct protein sequencing; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                  -> K (in Ref. 2).
-> T (in Ref. 2 and 4).
-> I (in Ref. 1).
                                                                 Phosphorylation; SH2 domain; Transcription regulation.
DOMAIN 580 670 SH2.
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25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
98.7%; Score 1157; DB 1;
Best Local Similarity 98.7%; Pred. No. 2.9e-65;
Matches 226; Conservative 1; Mismatches 2;
                                                                                                                                                                                    /FTId=VSP 006287
                                                                                                                  Phosphoserine
                                                                                                                                                                    Stat3B)
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01-OCT-1996 (Rel. 34, Last seq
25-OCT-2004 (Rel. 45, Last ann
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MOD_RES
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VARŜPLIC
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P52631;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on itse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs.ch/b.ch/.
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                                                                                                                                 "Transcription factors Stat3 and Stat5b are present in rat liver nuclei late in an acute phase response and bind interleukin-6 response
                                                                                                                                                                                                                                                                                                                                                                           ACUTE-Phase protein genes.

PATHWAY: Involved in the gp130-mediated signaling pathway.

PATHWAY: Involved in the gp130-mediated signaling pathway.

SUBNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOAI (By similarity).

SUBCELLUIAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation (By similarity).

FTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity (By similarity).

SIMILARITY: Belongs to the transcription factor STAT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACIGGPPNICLDRLENWITSLABSQLQTRQQIKKLBELQQKVSYKGDPIVQHRPMLBERI
                                                                                                                                                                                                                    elements.";
J. Biol. Chem. 270:29998-30006(1995).
-!- FUNCTION: Transcription factor that binds to the interleukin-6
(IL-6)-responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMBYVQKTLTDEELADWKRRQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NHPTAAVVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSS0001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998;
Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.5%; Score 1154; DB 1; Length 770; ilarity 98.3%; Pred. No. 4.5e-65; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UDLIFRILIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      705 705 Phosphotyrosine (by JAK) (By 727 727 Phosphoserine (By similarity) 770 AA; 88039 MW; D74AOC76954754ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, X91810; CAA62920.1; -.
HSSP; P42227, 1BG1.
RGD; J772; Stat3.
InterPro; IPR008967; P53 like_DNA_bnd.
InterPro; IPR001217; STAT.
Pfan; PF001017; STAT_alpha; 1.
Pfan; PF01017; STAT_alpha; 1.
Pfan; PF02865; STAT_int; 1.
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                                                                                                                                                                                                                  TISSUE-Mammary gland;

Greyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;

Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;

Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;

The STATS-encoding gene was flipped across the STAT3/STAT5A-locus

The Thuring ruminant evolution.";

Submitred (JAN-2004) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: Transcription factor that binds to the interleukin-6

- I- FUNCTION: Transcription factor that binds to the interleukin-6

- I- FUNCTION: Transcription factor with pathway.

- STBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).

- SUBCLIGUAR LOCATION: Cytoplasmic, translocated into the nucleus in response to phosphorylation (By similarity).

- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NHPTAAVVTEKOOMLEOHLODARKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphotyrosine (by JAK) (By similarity)
Phosphoserine (By similarity).
9CEB147C73E83274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.1%; Score 1150; DB 1; Length 770; 98.3%; Pred. No. 8.1e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                      05-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
Name-STAT3;
              770 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
              PRT;
                                           (Rel. 44, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ620655; CAF06182.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87974 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  franscription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 98.3
Matches 225; Conservative
              STANDARD;
                                                                                                                 Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              705 7
727 7
770 AA;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                           NCBI_TaxID=9913;
              BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310
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Q6DV79
ID Q6DV
AC Q6DV
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771 AA

PRELIMINARY;

06DV79 06DV79;

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191 NNQSVTRQKMQQLEQMLTALDQMRRGIVSELAGLLSAMEYVQKMLADEELADWKRRQQIA 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 NNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEIA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 CIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIV 181
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last amnotation update)
51-OCT-2004 (TrEMBLrel. 28, Last amnotation update)
51-OCT-2004 (TrEMBLrel. 28, Last amnotation 3.
63-101 (Chicken).
63-101 (Chicken).
64-101 (Chicken).
64-101 (Chicken).
65-101 (Chicken).
67-101 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asashima M., Yokota T.;
"Activation of Stat3 by cytokine receptor gpl30 ventralizes Xenopus embryos independent of BMP-4.";
Dev. Biol. 216.481-490(1999).
EMBL; AB017701; BAA86061.1;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Zhou G.Y., Leung F.C.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AY641397; AAT6487.1; -.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0004871; F:signal transducer activity; IEA.

GO; GO:000700; F:transcription factor activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0005555; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 771;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88174 MW; 71AC855C5DEC03E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1132; DB 2;
Pred. No. 1.1e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   769 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR008967; P53 like_DNA_bnd
InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00017; SH2; 1
Pfam; PF01017; SH2; 1
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02864; STAT_bind; 1.
PROSITE; PS550001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 221; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=stat 3;
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Best Local
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Q9PVX8
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DR GO; GO: 00005634; C: nucleus; IEA.

BR GO; GO: 00005634; C: nucleus; IEA.

BR GO; GO: 00004871; F: stagnal transducer activity; IEA.

BR GO; GO: 0000742; P: intracellular signaling cascade; IEA.

BR GO; GO: 0000742; P: intracellular signaling cascade; IEA.

BR GO; GO: 0000742; P: intracellular signaling cascade; IEA.

BR GO; GO: 00007435; P: regulation of transcription, DNA-dependent; IEA.

BR InterPro; IPR001980; SH2.

BR InterPro; IPR00197; STAT.

BR Ffam; PF0017; STAT.

BR Ffam; PF002864; STAT.

BR Ffam; PF02865; STAT.

BR Ffam; PF02865; STAT.

BR PROSITE; PS550001; SH2; 1.

BR PROSITE; PS550001; SH2; 1.

CEACURNCE 766 AA; 87599 MW; 31018A3321CCEB9C CRC64;
'Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIRKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NHPTAAVVTEKOOMLEQHLODARKRVODLEQKMKVVENLODDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
                                                                                                                            MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                       "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 93.5%; Score 1096; DB 2; Length 7 Best Local Similarity 91.7%; Pred. No. 2.1e-61; Matches 210; Conservative 11; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ databases
                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                             Klein S., Strausberg R.;
Submitted (JAN-2003) to the
EMBL; BC044717; AAH44717.1;
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26, Stat3 protein.
                                                                                                                                                                                                                                                     Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyprinidae; Danio
NCBI_TaxID=7955;
                        mouse cDNA
                                                                                                                                                                                                                               initiative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=stat3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310
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WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257; PubMed=1., Grouse L.H., Denmen C.M., Schuler G.D.,
MALSCHUL S.F., Zeeberg B., Buetow K.H., Shamen C.M., Schuler G.D.,
MALSCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
MALSCHUL S.F., Moore T., Max S.I., Wand J., Habie F.,
MARSCHUL M.J., Usdin T.B., Toshiyuki S., Carnino P., Prange C.,
MARA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
MARA S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
MALSCHUL S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
MILIAION D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Milialon D.K., Muzny D.M., Garcia A.M., Gay L.J., Hulyk S.W.,
Miling M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Miling M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Malakesley R.W., Touchman J.W., Green E.D., Myers R.M., Butterfield Y.S.,
Marack R.M., Malan M., Shalska U., Smailus D.E., Schnerch A., Schein J.E.,
Marack R.M., Malan M., Shalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFDYXKTLKSQGDMQDLN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
         GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:000720; F:transcription factor activity; IEA.
GO; GO:000724; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000896; F93_like_DNA_bnd.
InterPro; IPR001217; STAT.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                         Length 769;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                      769 AA; 87974 MW; 0905C03263303069 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                      Score 1099; DB 2;
Pred. No. 1.4e-61;
9; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
SMART; SM00252; STAT_int; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                         93.8%;
92.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 212; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stat3-A protein.
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SEQUENCE
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Q7ZXK3;
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Query Match
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alusner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Abtchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M. J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Scheid Y.S.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GG; GO:0005634; C:nucleus; IEA.
GG; GO:0004871; F:signal transducer activity; IEA.
GG; GO:0004871; F:signal transducer activity; IEA.
GG; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GG; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008967; P53 like_DNA_bnd.
InterPro; IPR0017; STAT.
IPR0 Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bnd; 1.
Pfam; PF02865; STAT_bnd; 1.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation factor 3.
Signal transducer and activation of transcription factor 3.
Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.3%; Score 1011; DB 2; Length 414; 84.8%; Pred. No. 2.7e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 IVDLFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO45276; AAH45276.1; --
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 195; Conservative
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130 HPTGTVVTEKQQILEHNLQDIRKRVQDMEQKMKMLENLQDDFDFVYKTLKSQGELNQDLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                               Liu R., Hong Y.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; AX639947; AAT64912.1; -
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:000555; P:regulation of transcription, DNA-dependent; IEA.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence second anotation update)
Signal transducer and activator of transcription 3 isoform 1.
Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Suteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AX641434, AAT46364.1;
GO, GO:0005634, C:nucleus; IEA.
GO, GO:0004871; F:signal transducer activity; IEA.
GO, GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:000735; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; P53_like_DNA_bnd.
InterPro; IPR001217; STAT.
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Acanthomorpha; Acanthopterygii; Percomòrpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
NCBI_TaxID=8090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 765;
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84.8%; Pred. No. 5.2e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR008967; P53_like_DNA_bnd.
InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
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Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT_int; 1.
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Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
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SEQUENCE 765 AA; 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7955;
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MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Bardenen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Bucher C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toobhlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcha A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garchen A.M., Gay L.J., Hulyk S.W.,

A Nollalon D.E., Retreman M., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Gones A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Goneration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                       Gaps
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
NCBI_TaxID=7955,
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                                                                                                                                                                         5
                                                                                                                Query Match

86.3%; Score 1011; DB 2; Length 785;
Best Local Similarity 84.8%; Pred. No. 5.3e-56;
Matches 195; Conservative 19; Mismatches 14; Indels 2
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Submitted (ARR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC068320; AAH68320.1; ...
ZRIN; ZDB-GRNE-980526-68; stat3.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
                                                           89643 MW; 81F231BDE27DE938 CRC64;
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Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Brachydanio rerio (Zebrafish) (Danio rerio)
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
Pfam; PF02864; STAT_bind; 1.
                         int; 1.
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                       Pfam; PF02865; STAT_in
PROSITE; PS50001; SH2;
SEQUENCE 785 AA; 89
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Thesis (1998), University of Melbourne, Australia.

EMBL' A4006693; CAA06677.1; -.

REMBL' A400693; CAA06677.1; -.

RESP, P42227; 1BG1.

RESP, P42227; 1BG1.

RESP, P62277; Fisignal transder activity; IEA.

GO; GO:000471; Fisignal transder activity; IEA.

GO; GO:000471; Fisignal transder activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0006555; P:requlation of transcription, DNA-dependent; IEA.

InterPro; IPR008967; P53 like_DNA_bnd.

InterPro; IPR0017; STAT.

Refam; PF0017; STAT alpha; 1.

Refam; PF0017; STAT alpha; 1.

Refam; PF0265; STAT int; 1.

SWART; SM0252; STAT int; 1.

SWART; SM0252; STAT; 1.

REPROSITE: PS5001; SH2; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR0018967; P32_like_DNA_bnd.
InterPro; IPR001980; SH2.
InterPro; IPR001217; STAT.
Pfam; PF001017; STAT.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_bind; 1.
Pfam; PF02865; STAT_bind; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Indels
                                                                                                                                                                                                                                                                                                                                                      90039 MW; FC7371D0B0E5447E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74BC4EA401C3C942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
86.3%; Score 1011; DB 2;
Best Local Similarity 84.8%; Pred. No. 5.4e-56;
Matches 195; Conservative 20; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.3%; Score 1011; DB 2;
84.8%; Pred. No. 5.5e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   806 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50001; SH2; 1.
806 AA; 92151 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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us-10-090-185-31.rup

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Match
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  RESULT 14
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 2
                                GNNO-SVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMBYVOKTLTDEELADWKRRPE 119
                                                                                                             IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                           250 IACIGGPPNICLDRLETWITSLAESQLQIRQQIRKLEELQQKVSYKGDPIIQHRPALEEK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                            HPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 HPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
 Gaps
                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P4227; 1BG1.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0004871; F:signal transducer activity; IEA.

GO; GO:0004871; F:signal transducer activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

Fram; PP00117; STAT_alpha; 1.

Pfam; PF01017; STAT_alpha; 1.

Pfam; PF02865; STAT_int; 1.
 2,
                                                                                                                                                         IVELPRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                   Length 764;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307106; AAL09415.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87411 MW; E661FFE18BEFD8BE CRC64;
                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.2%; Score 987; DB 2;
83.5%; Pred. No. 1.7e-54;
                                                                                                                                                                                                                                        764 AA.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Mismatches
                                                                                                                                                                                                                                                                                                        Tetraodon fluviatilis (Puffer fish)
20;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 192; Conservative
                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00252; SH2;
PROSITE; PS50001; SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       764 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                      ~
                                                                                                                                                         180
                                                                61
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Matches
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60 NGNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 EIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 QIACIGGPPKICLDRLETWITSLGBIQLQIRQIKKLBELQQKVSYKGDPIIQHRPALEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                          Name-rbtStat3;
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 RIVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007370; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MRA-2004 (TrEMBLrel. 26, Last annotation update)
Signal transducer and activator of transcription (Fragment)
Name=STAT3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Indels
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Johnson M.C., Mourich D.V., Leong J.C.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, 160333, AAB60926.1; -.
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Arredondo J.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR008967; P53 like_DNA_bnd.
InterPro; IPR001909; SH2_
InterPro; IPR01217; STAT.
Pfam; PF01017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bnd; 1.
Pfam; PF02865; STAT_bnd; 1.
SEQUENCE 767 AA; B7816 MW; PED97740C74C3798 CRC64;
                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 977; DB 2;
; Pred. No. 7.4e-54;
24; Mismatches 17;
Ä.
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                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 81.49
Matches 188; Conservative
                                      01-JUL-1997 (TrEMBLrel.
01-JUL-1997 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9544;
                                                                                                                                                                                                                                            NCBI_TaxID=8022;
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                                                                                                                                                                                                                                                                                                                                                                            1 VQKTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQK 60
               R HSSP; P42227; 1BG1.

R GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0005155; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:0007165; P:signal transduction; IEA.

R InterPro; IPR001957; P53 like_DNA_bnd.

R InterPro; IPR001977; STAT_alpha; 1.

R Pfam; PF01017; STAT_alpha; 1.

R Pfam; PF02664; STAT_bind; 1.

T NON TER.

1 163 163

C SEQÜENCE 163 AA; 18855 MW; DD3F11E7F5B9878C CRC64;
                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                            Query Match 56.0%; Score 656; DB 2; Length 163; Best Local Similarity 98.4%; Pred. No. 3.1e-34; Matches 126; Conservative 1; Mismatches 1; Indels
EMBL; AF227560; AAF73401.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 LLVKFPEL 229
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Search completed: May 25, 2005, 17:43:45 Job time: 96.284 secs